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Insights into Current Tropomyosin Receptor Kinase (TRK) Inhibitors: Development and Clinical Application

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Abstract: The use of kinase-directed precision medicine has been heavily pursued since the discovery and development of imatinib. Annually, it is estimated that around ~20,000 new cases of TRK-driven cancers are diagnosed, with the majority of cases exhibiting a TRK genomic rearrangement. In this perspective article, we discuss current development and clinical applications for TRK precision medicine by providing the following: (1) The biological background and significance of the TRK kinase family, (2) A compilation of known TRK inhibitors and analysis of their co-crystal structures, (3) An overview of TRK clinical trials, and (4) Future perspectives for drug discovery and development of TRK inhibitors.

Introduction

The tropomyosin receptor kinase (TRK) family of enzymes are transmembrane, receptor tyrosine kinases (RTK) that regulate synaptic strength and plasticity in the mammalian nervous system.¹⁻⁸ In this role, the TRK family regulates cell differentiation, proliferation, survival, and pain.⁹⁻²³ There are three members of the TRK family: TRKA (encoded by *NTRK1* gene), TRKB (*NTRK2*), and TRKC (*NTRK3*), which have all been implicated to drive initiation and progression of malignancies.²⁴⁻⁴¹ Similar to the BCR-ABL gene fusion product that drives chronic myelogenous leukemia (CML),⁴² *NTRK* rearrangements and fusion gene products have been observed in numerous tumor types, which has been comprehensively reviewed by Vaishnavi, *et al* and Amatu, *et al*.⁴³⁻⁴⁴ Unlike CML, however, the incidence of *NTRK* fusion genes in each specific tumor type overall is rare. This generates profound difficulties for patient identification and adequate recruitment for clinical trials. For instance, *NTRK2* gene fusions have been identified in 0.2% of lung adenocarcinoma,⁴⁵ which represents approximately 184 patients of 92,138 diagnosed in 2010 in the USA.⁴⁶ On the other end of the spectrum, *NTRK3* fusion genes have been identified in virtually all secretory breast carcinomas and of mammary analogue secretory carcinomas (MASC), an extremely rare tumor of the salivary (in general, of the parotid) gland.⁴⁷ In fact, the defining characteristic of MASC, when compared to other salivary carcinomas, is an *NTRK* gene fusion.⁴⁷ In addition, *NTRK* fusions are found in about 50% of pediatric diffuse intrinsic pontine glioma and non-brainstem glioblastoma.⁴⁸ In major cancer subgroups, *NTRK* fusions occur in 3.3% of lung cancers,^{45,49} 2.2% of colorectal cancers,^{45,49-52} 16.7% of thyroid cancers,^{45,53-54} 2.5% of glioblastomas, and 7.1% of pediatric gliomas.^{43,55} Finally, similar to the receptor tyrosine kinase RET (rearranged during transfection), *NTRK* fusions (particularly ETV6-*NTRK3*) are common in post-Chernobyl radiation-induced papillary thyroid carcinomas.⁵⁶⁻⁵⁷ Thus, targeting TRK oncogenes is an attractive therapeutic approach for a diverse, frequently rare set of cancers.

The primary method to target TRK oncogenes is the use of small molecule kinase inhibitors. Because gene fusion products are the major oncogenes observed, other targeting strategies, such as antibody therapy, will not be effective since transmembrane tyrosine kinase fusions frequently lack an extracellular domain.⁵⁸ In this case, the fusion proteins are only susceptible to small molecule inhibition.⁵⁹⁻⁶¹ In general, small molecules are designed to target the adenosine triphosphate (ATP) binding site of TRK to block catalytic activity. This is based on the principle that protein kinases catalyze a phosphoryl transfer to a downstream substrate and only have micromolar affinity for ATP.⁶² Since turnover is rapid and

kinase affinity for ATP is weak, small molecules can effectively bind and inhibit TRK despite a high cellular concentration of ATP. Because of the druggability of the TRK enzyme class, a number of attempts to target TRKs have been completed. In this perspective article, we discuss current development and clinical application of TRK-targeted cancer therapy including (1) The biological background and significance of the TRK family, (2) A compilation of known TRK inhibitors and analysis of TRK/inhibitor co-crystal structures, (3) An overview of TRK clinical trials, and (4) Future perspectives for drug discovery and development of TRK inhibitors.

TRK Biology and Signaling

The TRK oncogene was initially discovered in colon cancer in which the cytoskeletal protein tropomyosin was fused to an unknown, catalytically active kinase domain.^{50,63} Further studies identified the kinase as a single-pass receptor tyrosine kinase expressed in the developing central nervous system and was given the name tropomyosin receptor kinase. In the extracellular region of TRK, there is a leucine rich motif, two cysteine-rich domains, and two immunoglobulin-like domains and all are essential for ligand recognition and binding.⁶⁴⁻⁶⁶ Unlike typical RTKs, the TRK intracellular region is small and comprised of roughly 70 amino acids before and 15 amino acids after the kinase domain.⁶⁴⁻⁶⁵ In comparison to other RTKs, TRK is most similar to the insulin receptor and has been implicated in insulin signaling.⁶⁷

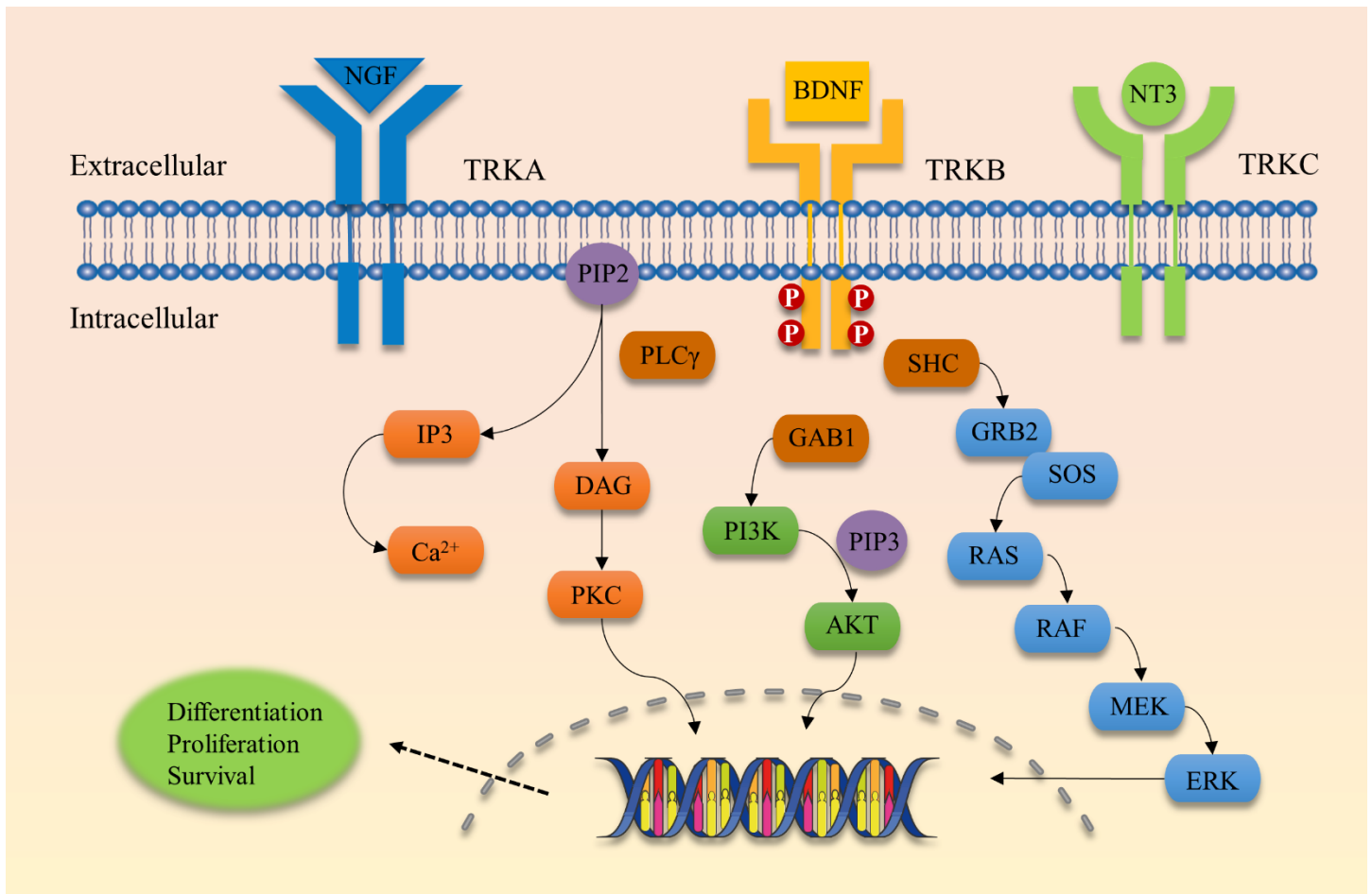


Figure 1. Schematic view of TRK receptor tyrosine kinases and major signal transduction pathways involved in cell differentiation, proliferation, and survival. TRKA is activated by nerve growth factor (NGF), TRKB is activated by brain-derived neurotrophic factor (BDNF), and TRKC is activated by neurotrophin-3 (NT3). RAS, rat sarcoma oncogene; RAF, rapidly accelerated fibrosarcoma oncogene; MEK, mitogen-activated protein kinase; ERK, extracellular signal-regulated kinase; GRB2, growth factor receptor-bound protein 2; SHC, SRC homology 2 domain containing; PI3K, phosphatidylinositol-4,5-bisphosphate 3-kinase; AKT, v-AKT murine thymoma viral oncogene homologue; PLC γ , phospholipase C- γ ; DAG, diacyl-glycerol; PKC, protein kinase C; IP3, inositol trisphosphate.

The TRK family is comprised of three distinct isoforms: TRKA, TRKB, and TRKC. A major difference between all three isoforms is the ligand that activates the receptor. TRKA is activated by nerve growth factor (NGF),⁶⁸⁻⁷⁰ TRKB is activated by brain-derived neurotrophic factor (BDNF),⁶⁹⁻⁷⁰ while TRKC is primarily activated by neurotrophin 3 (NT3) (Figure 1).⁷¹⁻⁷² The kinase domains of TRKA, TRKB, and TRKC share between 72% and 78% sequence identity.⁷³ When looking at the residues that interact directly with ATP in the active site,⁷⁴ TRKA and TRKB share 95% sequence identity

while TRKB and TRKC are completely identical.⁷³ In the TRK domain, the TRKA hinge is more structurally constrained compared to TRKB and TRKC, suggesting the hinge environment differs between TRK isoforms.⁷⁴ Further, the kinase insert domain of the TRK family is not structurally conserved, which is another key difference within the family.⁷⁴

Similar to the RTK superfamily, TRKs dimerize in response to ligand binding (Figure 1 and 2).⁷⁵ After ligand binding, TRKs autophosphorylate each monomer followed by rapid phosphorylation of the kinase activation loop.⁷⁶⁻⁷⁸ These phosphorylation events enhance catalytic activity of the kinase. To generate attachment sites for adapter proteins, the NPXY motif (Y490 in TRKA) in the juxtamembrane domain and the YLDIG motif (Y785 in TRKA) in the carboxy terminus are phosphorylated.⁷⁹⁻⁸² These phosphorylation events create docking sites for SRC Homology Domain 2 (SH2) and Phosphotyrosine binding domain (PTB) containing proteins, such as SHC and phospholipase C-gamma (PLC-gamma). After binding, SHC and PLC are activated through TRK-catalyzed phosphorylation.^{44, 83}

SHC was the first adaptor protein identified to bind to the phosphorylated NPXY motif of TRK, which results in the activation of the AKT and RAS canonical pathways.^{80-82, 84} After SHC is activated, a secondary adaptor protein, growth factor receptor-bound protein 2 (GRB2),⁸⁵ is recruited and facilitates GTP-loading of RAS via the guanine nucleotide exchange factor, SOS.⁸⁶ The activated, GTP-bound form of RAS activates the MAP kinase cascade, which includes activation of RAF, MEK, and ERK.⁸⁷ The ERK kinase translocates into the nuclear membrane activating transcription of target genes involved in cell growth, survival, and proliferation.⁸⁸

Activation of the AKT pathway occurs via recruitment of SHC and GRB2 to the NPXY motif of TRK, which signals through the intermediary molecule, GRB2-associated-binding protein 1 (GAB1). This stimulates activity of phosphoinositide 3-kinase (PI3K) leading to phosphorylation of PI4,5 lipids at the 3'-position.⁸⁹ On AKT, there is a conserved pleckstrin homology (PH) domain, which interacts with the 3'-phosphorylated lipids leading to AKT activation.⁹⁰⁻⁹³ AKT activation leads to increased expression of cell survival and proliferation genes that enhance pro-survival phenotypes mediated through TRK receptors.⁹⁴⁻⁹⁸

TRK Implication in Cancer

Genetic mutations in the TRK family have been reported in many cancers, namely carcinomas of the colon, thyroid, lung, ovary, breast (secretory breast carcinoma), salivary gland (mammary analogue secretory carcinoma),

pancreas, melanoma, spitzoid neoplasms, cholangiocarcinoma, stromal tumors (congenital fibrosarcoma, congenital mesoblastic nephroma, soft tissue sarcoma, gastrointestinal stromal tumor, inflammatory myofibroblastic tumor), brain tumors (pediatric glioma, astrocytoma and glioblastoma) and leukemia (Table 1 and Figure 3).^{43, 99-100 49, 51, 53, 57, 101} Within the TRK family, TRKA is the most commonly identified oncoprotein, which is found at a rate of approximately 7.4% across multiple tumor types.⁴³ Following is TRKC and then TRKB, which are found at rates of 3.4% and 0.4%, respectively. The majority of TRKB mutations have a frequency of less than 0.5% and many TRKC mutations have a frequency of less than 1.0%.⁴⁹

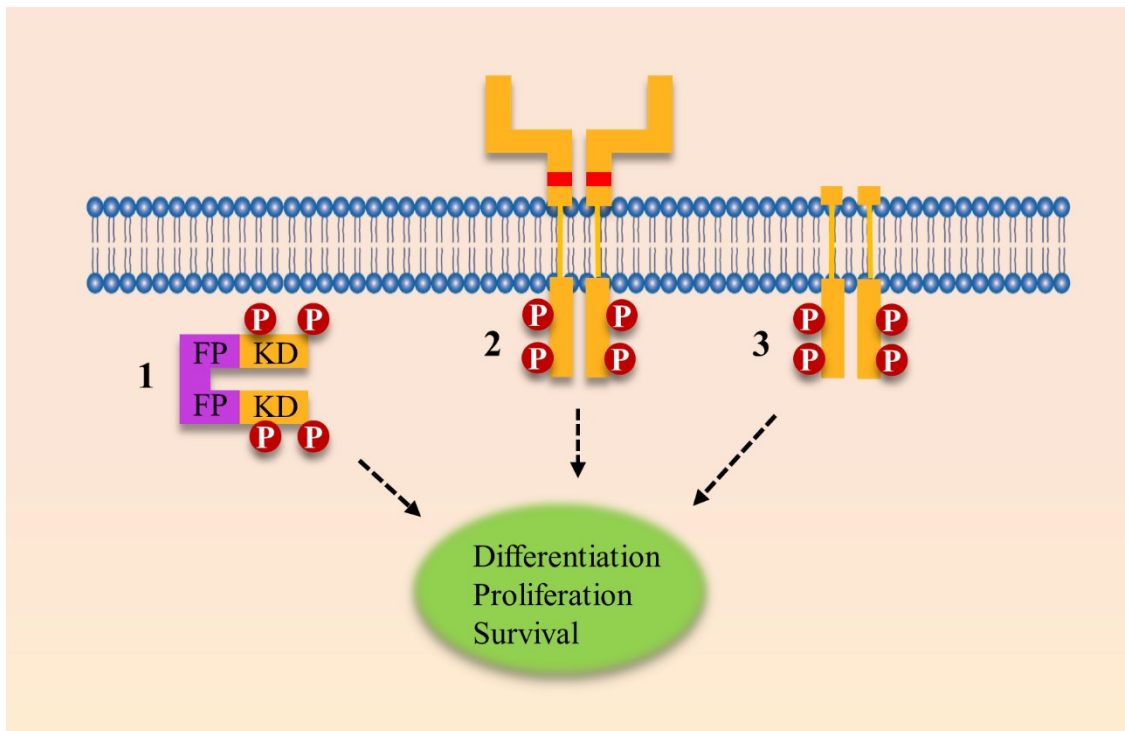


Figure 2. Ligand-independent signaling leading to constitutive TRK activation can occur through three, distinct mechanisms: A genomic rearrangement event; Extracellular point mutations; or Truncations of the extracellular domain. (1) In a genomic rearrangement event the kinase domain of TRK is fused to an unrelated protein, typically called the fusion partner. In this example, a cytoplasmic chimeric TRK fusion is shown without the transmembrane (TM) domain. Of note, TRK fusions can occur with or without the TM domain.¹⁰² (2) Point mutations can occur in the extracellular domain of TRK, generating a TRK oncogene with transforming abilities. Point mutations that are transformative under laboratory conditions have been identified at P203A and C345S.¹⁰³⁻¹⁰⁴ (3) Through in-frame deletions and alternative

splicing events, the TRK kinase can present with a truncated extracellular domain. These aberrant gene products have been identified in AML and neuroblastoma.¹⁰⁵⁻¹⁰⁷ FP: fusion partner. KD: kinase domain.

When an *NTRK* gene fusion occurs, the translocation event generates a hybrid oncogene composed of the active TRK kinase domain linked to an unrelated gene or fusion partner, triggering constitutive activation or overexpression of the TRK protein (Figure 2).^{44, 53} The resulting aberrantly expressed, novel oncogene can occur with or without the transmembrane domain.^{43, 102} Certain mutations in the extracellular domain of TRKA, namely P203A and C345S, have been identified as transforming under laboratory conditions but have yet to be identified in human tumor samples.¹⁰³⁻¹⁰⁴ On the other hand, in-frame deletions (Δ TRKA) and splice variants (TRKAIII) of *NTRK1* have been functionally identified and characterized in human tumor samples.^{52, 105-107} The Δ TRKA in-frame deletion, identified in acute myeloid leukemia (AML), contains a truncated extracellular domain that can transform both epithelial and fibroblast cells.¹⁰⁷ The TRKAIII splice variant, identified in neuroblastoma, has deletions in exons 6, 7, and 9, which results in the loss of Ig-like C2-type I (IG-C2) and glycosylation sites in the extracellular domain (Figure 2).^{52, 106} TRKA activating mutations from either genomic rearrangements, point mutations, deletions, or splice variants compromise the ability to regulate the kinase domain. This suggests that a key attribute to the oncogenic potential of TRK is the loss of the extracellular domain and/or its function.

Table 1. Oncogenic TRK fusions are found across multiple tumor types^a

Cancer Site	Estimated US Cases / yr	TRKA%	TRKB%	TRKC%
Lung Adenocarcinoma (NSCLC)	92,138 ⁴⁶	3.3 ⁴⁹	0.2 ⁴⁵	/
Colorectal	135,430 ¹⁰⁸	1.5 ^{49-50, 52, 51}	/	0.7 ⁴⁵
Intrahepatic cholangiocarcinoma	2,970 ¹⁰⁹⁻¹¹⁰	3.6 ¹¹¹	/	/
Papillary thyroid cancer	45,496 ^{108, 112}	12.3 ⁵³	/	14.5 ^{54, 113}
Glioblastoma	11,376 ^{108, 114}	1.25 ^{55, 115}	/	/
Head and neck squamous cell carcinoma	63,030 ¹¹⁶	/	0.2 ⁴⁵	0.2 ¹¹⁷
Mammary analogue secretory carcinoma	151 ^{108, 118}	/	/	100 ¹¹⁹
Ph-like acute lymphoblastic leukemia	1,192 ¹²⁰⁻¹²¹	/	/	0.7 ¹²²
Acute myeloid leukemia	15,976 ^{121, 123}	/	/	0.0125 ^{57, 124}

Skin cutaneous melanoma	87,110 ¹²¹	/	/	0.3 ⁴⁵
Secretory breast carcinoma	252 ^{121, 125}	/	/	92 ¹²⁶
Estimated Total Cases / yr		10,917	310	8,325
Estimated Percent of Cases / yr		55.8%	1.6%	42.6%

^a Only positive studies are listed, and thus the actual prevalence may be lower than reported.

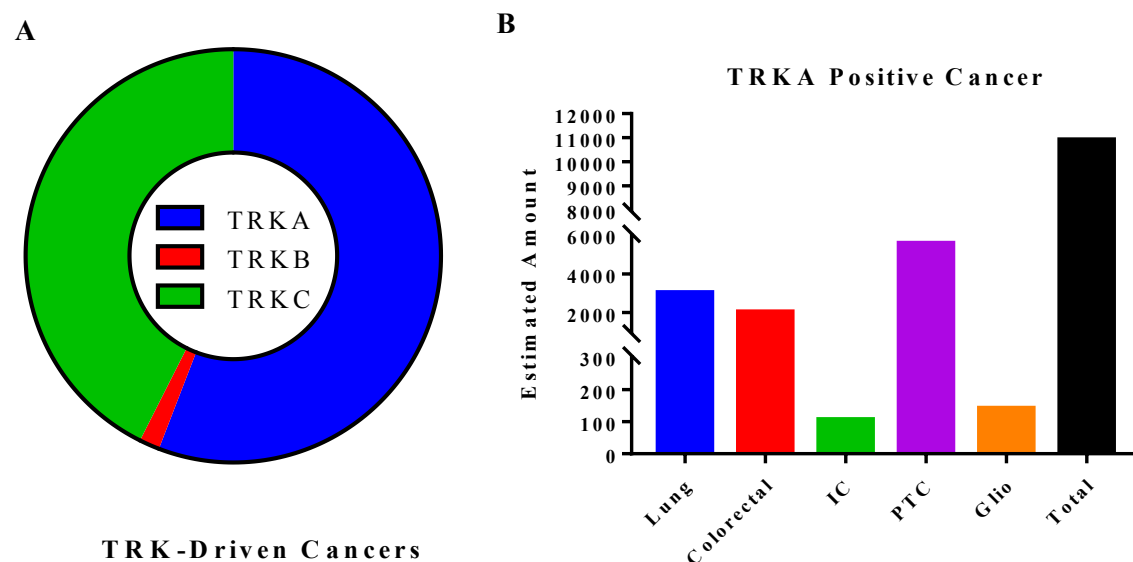


Figure 3: (A) Estimated contribution of TRKA/B/C mutations to all TRK-driven malignancies. Data is based on estimated incidence of cancers at major sites and contribution of TRK mutations at each site. It is estimated that a total of 19,552 cancers are diagnosed each year that have a TRK oncogene. Of the new cases, 55.8% (10,917) are TRKA, 42.6% are TRKC (8,325) and 1.6% (310) are TRKB. Because of the limited sequencing data, the actual amount of TRK-driven tumors could be significantly greater or lower depending on robustness of sample size, sample selection, and data analysis. Also, tumors with a TRK mutation could be dependent on a separate pathway. (B) Estimated number of cancers positive for TRKA. Lung (lung adenocarcinoma), IC (intrahepatic cholangiocarcinoma), PTC (papillary thyroid cancer), and Glio (glioblastoma).

In the tumor environment, TRK oncogenes stimulate uninhibited signaling through the RAS/RAF and PI3K/AKT pathways^{49, 127-129}. The preferred signaling cascade is cell-specific, with dominance from the RAS/RAF pathway observed in both colorectal (KM-12) and lung (CUTO-3) cancers. In certain cell types, TRK oncogenic signaling also occurs through the PI3K/AKT and STAT3 signal transduction pathways⁴⁹, and in other cases the RAS/RAF and PI3K/AKT

cascades are activated in concert.¹³⁰ Because of multifaceted pathway activation, TRK oncogenes are potent and highly oncogenic by stimulating both antiapoptotic and proliferative pathways.¹³¹ Further, TRK fusion oncogenes have been identified as important mediators to stimulate early tumor progression.¹³² Taken together, inhibition of TRK oncogenes can have chemotherapeutic and chemopreventive effects and, subsequently, has become a hotbed for therapeutic discovery efforts. In this perspective, we summarize TRK inhibitors from peer-reviewed literature; compounds from patents have been previously reviewed by McCarthy and Bailey *et al.*¹³³⁻¹³⁵

TRK Inhibitors

The following section represents a comprehensive overview of known TRK inhibitors and their corresponding discovery and development efforts. Because most TRK-activating mutations alter or eliminate the extracellular domain,⁵⁹⁻⁶¹ antibodies directed at TRK or TRK growth factors will not be effective as anticancer agents. Thus, all inhibitors reviewed are small-molecule kinase inhibitors that primarily target the TRK kinase domain. The inhibitors are at various stages of development from exploratory research, pre-clinical research, to clinical trials. Inhibitors have been classified based on their interactions with TRK¹³⁶ and are presented according to their binding modes. TRK inhibitors can be broken down into four, distinct subtypes based on ligand/binding interactions. The classifications are (A) Type I, (B) Type II, (C) Type III, and (D) Type IV.¹³⁷ (A) Type I TRK inhibitors are ATP competitive and bind to the ATP-binding site. The majority of TRK inhibitors under clinical investigation are Type I. (B) Type II TRK inhibitors are ATP non-competitive and exhibit non-competitive or *pseudo*-competitive binding kinetics. Type-II inhibitors bind at the ATP-binding site and also to an adjacent allosteric pocket. Only a subset of kinases permit such binding, including TRK, a binding mode which can be incorporated into compound design to increase selectivity. (C) Type III TRK inhibitors bind to the kinase domain outside of the ATP-binding site. Unlike Type II inhibitors, Type III inhibitors are true allosteric inhibitors and can exploit unique, kinase-specific functionality to help achieve selectivity among TRK isoforms. (D) Type IV TRK inhibitors bind to a region other than the kinase domain. The majority of kinases are expressed as multi-domain proteins with a catalytic domain and a regulatory domain. Type IV inhibitors can interrupt key protein-protein interactions or ligand interactions that limit activity of the kinase domain.¹³⁸ Because TRK genomic rearrangements often pair the TRK kinase domain to an

unrelated gene, it is unclear how effective the anticancer properties will be for Type IV TRK inhibitors. Type IV TRK inhibitors are not reviewed in this perspective.

Type I TRK Inhibitors

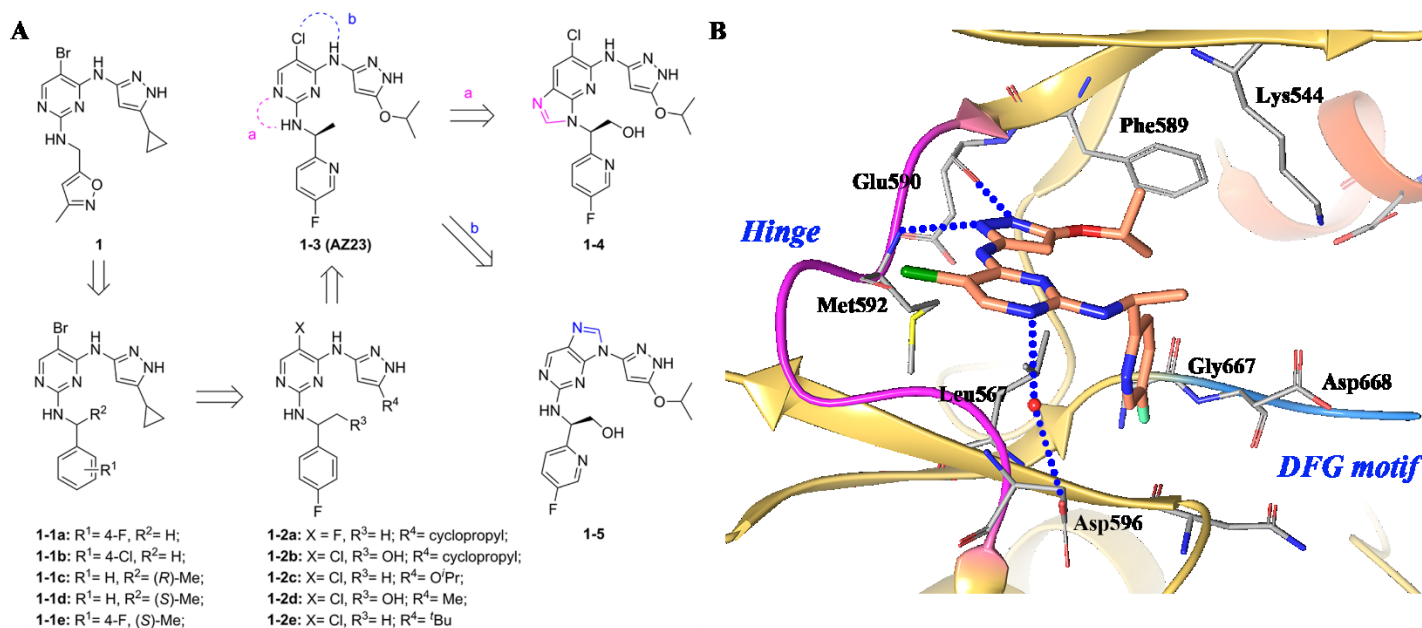


Figure 4. (A) Identification of compounds **1-3**, **1-4**, and **1-5**; (B) Co-crystal structure of compound **1-3** in TRKA (PDB ID: 4AOJ, 2.75 Å). The kinase is depicted in yellow ribbons and the hydrogen bonds are illustrated in blue dashed lines.

Type-I TRK inhibitors exhibit vast diversity in compound architecture, which will alter activity and selectivity profiles of the compounds. This helps to better define chemical space that is relevant to TRK inhibition and suggests points of refinement for future drug discovery efforts. Wang *et al* reported 4-aminopyrimidines with TRK inhibitory activity from a high throughput screening effort against TRKB (Figure 4A).¹³⁹ The group discovered compound **1** with activity on TRKA and B (IC₅₀ = 0.27 μM and 1.1 μM, respectively). To complete SAR studies on **1**, the isoxazole was replaced with a phenyl group, and halogen substitution at the 4-position of phenyl was found to improved potency (**1-1a** and **1-1b**, TRKA IC₅₀s were 0.10 μM and 0.36 μM, respectively).¹³⁹ SAR studies at R² indicated that the (S)-enantiomer is preferred over the (R)-enantiomer (**1-1c** vs **1-1d** and **1-1e**, TRKA IC₅₀s were 0.65 μM vs 0.10 μM and 0.006 μM, respectively). On the pyrimidine ring system, substituting bromine to fluorine or chlorine had little effect on TRKA activity (**1-2a** and **1-2b**, TRKA IC₅₀s were 0.017 μM vs 0.004 μM, respectively).¹³⁹ Replacement of cyclopropyl at R⁴

with isopropoxy is tolerated (**1-2c**, TRKA IC_{50} = 0.006 μ M), but altering aliphatic length or bulk decreases potency likely from geometric constraints at the TRKA hinge region (**1-2d** and **1-2e**, TRKA IC_{50} s were 0.081 μ M and 3 μ M, respectively). Further optimization and refinement strategies furnished orally bioavailable compound **1-3** (**AZ23**).¹³⁹ Compound **1-3** was active against TRKA and B (IC_{50} = 0.002 μ M and 0.008 μ M, respectively) and exhibited anticancer activity by oral dosing in a TRKA-driven allograft model and TRK-expressing xenograft model of neuroblastoma.¹⁴⁰ In 2012, a ring fusion study of this scaffold was reported by the same research group.¹⁴¹ Two different ring fusion strategies were employed to generate imidazo[4,5-*b*]pyridine and purine derivatives. Representative compounds of the two scaffolds, **1-4** and **1-5**, exhibited potent TRK inhibition. Both compounds displayed IC_{50} values of 0.0005 μ M against TRKA-dependent MCF10A cells (MCF10A-TRKA- Δ), and were also active in mice bearing 3T3-TRKA- Δ tumors.¹⁴¹

In the co-crystal structure of compound **1-3** with TRKA (Figure 4B), TRKA is found in an inactive conformation with the C-helix pushed into a non-catalytically active orientation.¹⁴¹ Compound **1-3** forms two hydrogen bonds at the hinge region with the pyrazole-moiety, and interacts with the amide backbone of Glu590 and Met592. The isopropoxy group is oriented toward Phe589, which is the gatekeeper amino acid. The fluoropyridine ring engages in an interaction with Leu657, and the fluorine atom is in close proximity to Gly667.¹⁴² Numerous TRK kinase inhibitors exploit this region to increase selectivity and potency.¹⁴¹ Based on the crystal structure, compound **1-3** is a Type-I kinase inhibitor.

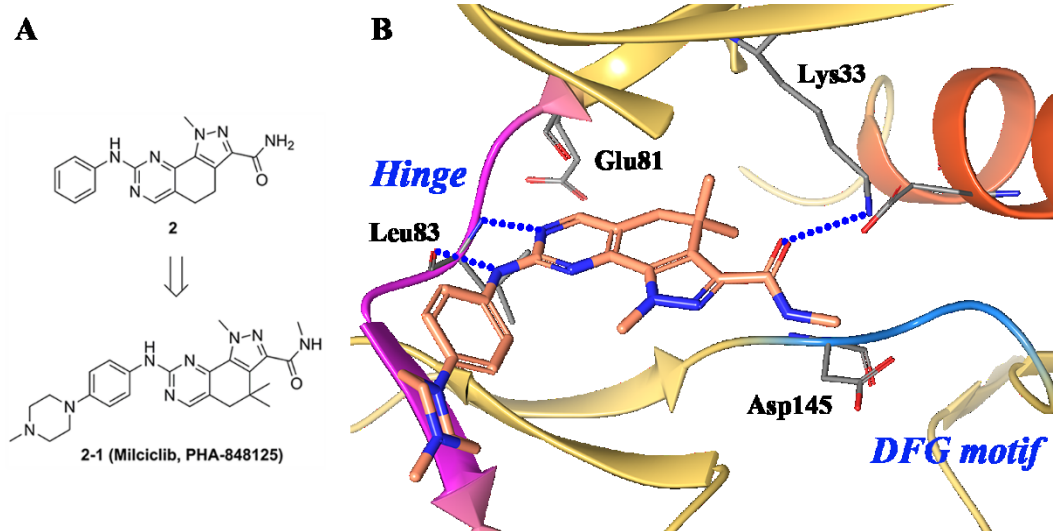


Figure 5. (A) Identification of **2-1**; (B) Co-crystal structure of compound **2-1** in CDK-2/cyclin A. (PDB ID: 2WIH, 2.5 Å). The kinase is depicted in yellow ribbons, and the hydrogen bonds are illustrated in blue dashed lines.

Further exploration of Type-I TRK inhibitors was reported by Brasca *et al.*¹⁴³ The group initially identified compound **2** as a potent CDK-2 (cyclin dependent kinase) inhibitor (Figure 5A).¹⁴³ Enhancement in selectivity, antiproliferative activity, and optimization of the physiochemical and pharmacokinetic properties led to the identification of compound **2-1** (**Milciclib, PHA-848125**) (Figure 5A) with high potency (CDK-2 IC_{50} = 0.045 μ M) and high bioavailability (F = 85%). Serendipitously, this compound exhibited near equal potency against TRKA (IC_{50} = 0.053 μ M) with selectivity in the greater kinome (IC_{50} s > 0.15 μ M).¹⁴³

Figure 5B illustrates the crystal structure of compound **2-1** in complex with CDK2/cyclin A.¹⁴³ The compound binds in the ATP pocket of the kinase with the pyrazoloquinazoline ring system occupying the adenine region, while the phenyl moiety points toward the solvent accessible region. Compound **2-1** creates two hydrogen bonds with the protein backbone of the hinge with residue Leu83. The amide carbonyl group of **2-1** is within hydrogen bonding distance of the conserved lysine (Lys33).¹⁴³

Albanese *et al.* further evaluated the dual inhibitory activity of compound **2-1** against CDK-2 and TRKA.¹⁴⁴⁻¹⁴⁵ *In vitro*, **2-1** was able to inhibit NGF-induced phosphorylation of TRKA as well as downstream signaling in the DU-145 human prostate carcinoma line. *In vivo*, **2-1** inhibited tumor growth in a human prostate DU-145 xenograft model in a dose dependent manner. Because of the dual inhibitory properties of **2-1**, the compound shifts the paradigm for precision medicine. Instead of generating a ‘magic-bullet’ with high TRK kinase selectivity, Albanese *et al.* focused on validating and developing a ‘smart-bomb’ with activity on the oncogene lesion (TRK) paired with cell cycle inhibition (CDK).¹⁴⁶

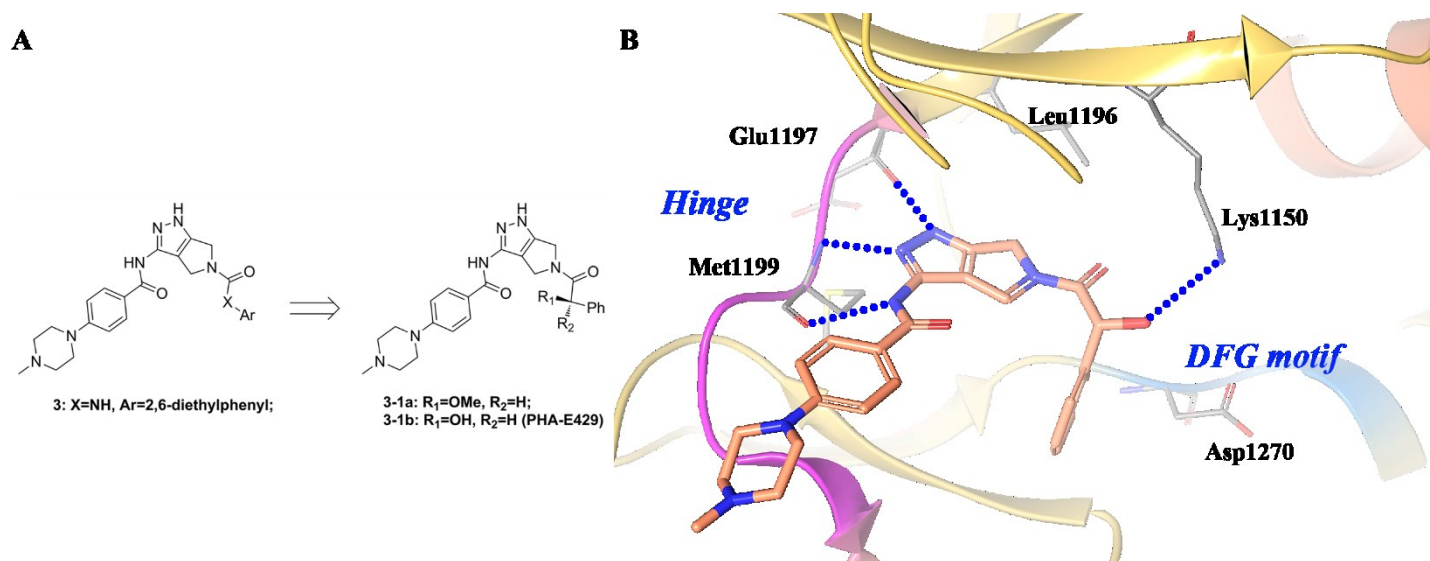


Figure 6. (A) Identification of compound **3-1b**; (B) Co-crystal structure of compound **3-1b** with ALK (PDB ID: 2XBA, 1.95 Å). The kinase is depicted in yellow ribbons, and the hydrogen bonds are illustrated in blue dashed lines.

In line with developing TRK inhibitors with dual activity, Fancelli *et al.* identified a series of 5-phenylacetyl 1,4,5,6-tetrahydropyrrolo[3,4-*c*]pyrazole as Aurora kinase inhibitors (compound **3**, Aurora-A IC₅₀ = 0.027 μM) (Figure 6A).¹²¹ Further medicinal chemistry efforts lead to the discovery of compound **3-1b**. Compound **3-1b** was found to have dual activity on TRKA (IC₅₀ = 0.03 μM) and Aurora A (IC₅₀ = 0.013 μM)¹²¹ with weak ALK (anaplastic lymphoma kinase) inhibitory activity (IC₅₀ = 0.091 μM).¹⁴⁷ Akin to **2-1**, compound **3-1b** obtained dual activity on the oncogene lesion (TRKA) as well as cell cycle inhibition (Aurora A).¹⁴⁷

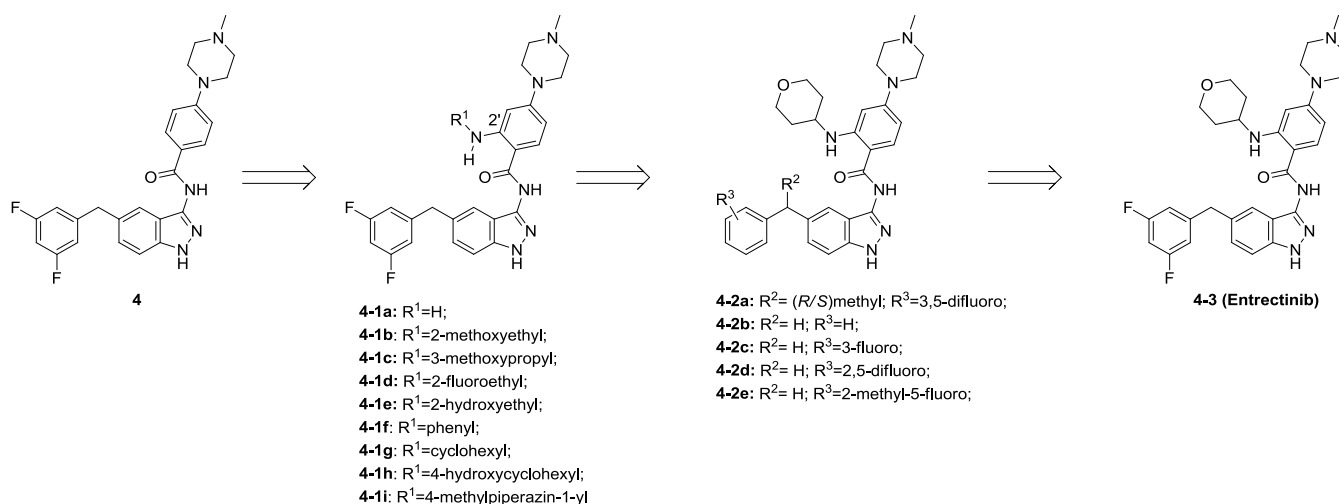


Figure 7. Structural optimization from compound **4** to **4-3**.

Recently, Menichincheri *et al.* disclosed research efforts to generate compound **4-3** (**Entrectinib**, **RDX-101**) for ALK ($IC_{50} = 0.012 \mu M$) (Figure 7).¹⁴⁸ To develop ALK inhibitors from compound **4** (ALK $IC_{50} = 0.073 \mu M$), the co-crystal complex of ALK with compound **3-1b** was studied (see Figure 6B).¹⁴⁸ Analysis of the complex suggested that a mono-substitution at 2'-position would generate derivatives that occupy the ATP sugar pocket region while simultaneously displacing a water molecule. In addition, NH-R substituents at this position were able to stabilize the bioactive conformation through intramolecular hydrogen bonding. Based on this concept, different amines were attached to the 2'-position of the central phenyl ring.¹⁴⁸

The introduction of a primary amine at 2' led to compound **4-1a** with similar ALK potency ($IC_{50} = 0.067 \mu M$).¹⁴⁸ This was consistent with modeling analysis as compound **4-1a** lacked the substituent necessary to fill the sugar pocket. At R^1 , a methoxyethyl or methoxy propyl group generally led to a moderate loss in activity (**4-1b**, and **4-1c**, ALK $IC_{50} = 0.21 \mu M$ and $0.135 \mu M$, respectively) while a fluorine or a hydroxyl group increased activity (**4-1d**, and **4-1e**, ALK $IC_{50} = 0.014 \mu M$ and $0.026 \mu M$, respectively).¹⁴⁸ On the contrary, phenyl or cyclohexyl significantly decreased affinity because of size constraints of the sugar pocket (**4-1f**, and **4-1g**, ALK $IC_{50} = 0.684 \mu M$ and $0.56 \mu M$, respectively).¹⁴⁸ Interestingly, introduction of a hydroxyl group furnished **4-1h** of which the *trans*-isomer displayed 10-fold higher activity (ALK $IC_{50} = 0.01 \mu M$) than the *cis*. When R^1 is 4-amino-N-methylpiperidinyl (**4-1i**) or 4-aminotetrahydropyranyl (**4-3**), the resulting compounds exhibit excellent potency on ALK ($IC_{50} = 0.015$ and $0.012 \mu M$, respectively). The latter of the two had better cellular activity (Cell $IC_{50} = 0.438 \mu M$ vs $0.031 \mu M$), which might be due to a difference in cell permeability.¹⁴⁸ Introduction of a methyl group to R^2 generated two enantiomers (**4-2a**), with one enantiomer being 3-fold more active than the other (ALK $IC_{50} = 0.059 \mu M$ and $0.019 \mu M$, respectively, absolute configuration not determined).¹⁴⁸ Due to labor-intensive chiral separation and stability of the benzhydryl stereogenic center further development of these compounds was terminated. Strong electron withdrawing groups on the phenyl ring are crucial for ALK activity. Removing the 3,5-difluoro substitution, changing the position of the fluorine, or replacing with methyl all decreased activity (Compounds **4-2b** to **4-2e**, ALK $IC_{50} = 0.106 \mu M$, $0.03 \mu M$, $0.038 \mu M$, $0.181 \mu M$, respectively).¹⁴⁸

After initial development for ALK, compound **4-3** was subsequently found active on ROS1 ($IC_{50} = 0.007 \mu M$) and TRK (IC_{50} s for TRKA/B/C were $0.001 \mu M$, $0.003 \mu M$ and $0.005 \mu M$, respectively).¹⁴⁸⁻¹⁴⁹ In antiproliferative studies, compound **4-3** was active against the colorectal cancer cell line KM-12 ($IC_{50} = 0.0017 \mu M$) and also induced tumor stabilization (>90% TGI) when administered P.O. to mice bearing KM-12 xenografts.¹⁵⁰ Compound **4-3** is currently in clinical trials for the treatment of patients with ALK-, ROS1- and TRK-dependent tumors and is exhibiting remarkable signs of efficacy.¹⁴⁸⁻¹⁴⁹ In a Phase 2 clinical trial, **4-3** is being investigated for advanced or metastatic solid tumors that harbor TRKA/B/C, ROS1, or ALK gene rearrangements (NCT02568267).

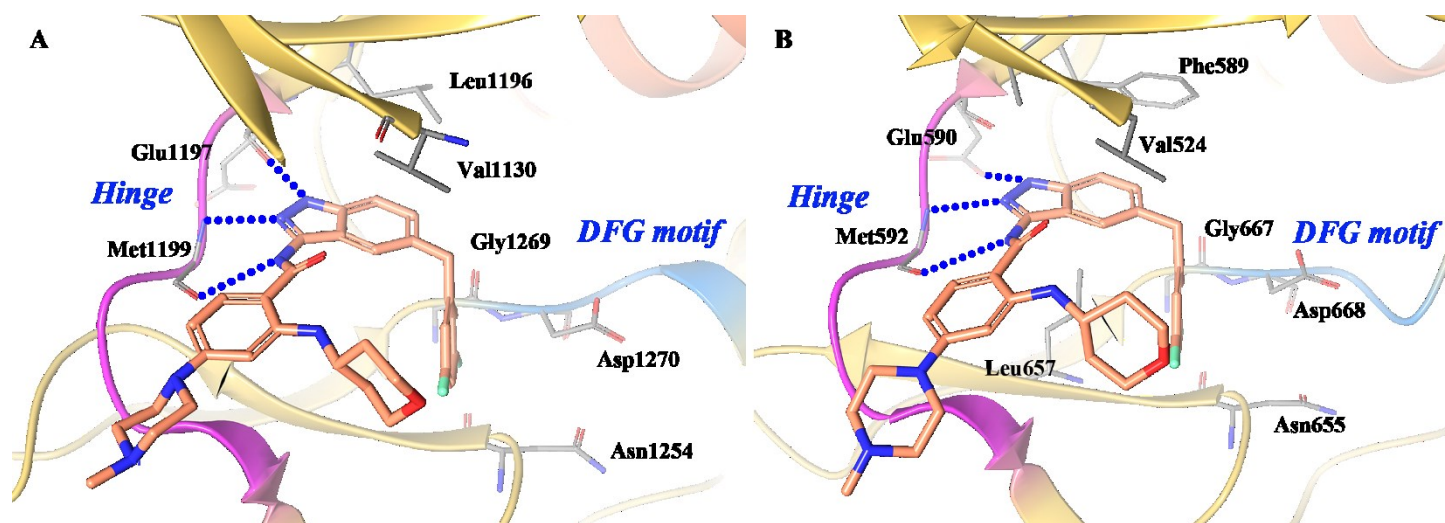


Figure 8. (A) Co-crystal structure of compound **4-3** with ALK (PDB ID: 5FTO, 2.22 Å): (B) Co-crystal structure of compound **4-3** with TRKA (PDB ID: 5KVT, 2.45 Å). The kinase is depicted in yellow ribbons, and the hydrogen bonds are illustrated in blue dashed lines.

The co-crystal structure of ALK with compound **4-3** was consistent with the above expectations (Figure 8A).¹⁴⁸ A similar binding mode is observed in the co-crystal structure of **4-3** with TRKA (Figure 8B).¹⁵¹ The compound is anchored to the hinge through three hydrogen bonds between the aminoindazole moiety and the backbone of residues Glu590 and Met592 (Glu1197 and Met1199 in ALK). The difluorobenzyl-indazole core creates favorable contacts with Ala542, Leu657 (Leu1256, and Val1130 in ALK), and the gatekeeper Phe589 (Leu1196 in ALK).¹⁴⁸ Moreover, the 3,5-difluorobenzyl moiety is involved in multiple interactions with the backbone carbonyls of Asp668 from the DFG motif (Asn1254 and Gly1269 in ALK). The central phenyl ring makes a hydrophobic contact with Leu516 (Leu1122 in ALK);

while the methylpiperazine is oriented towards the solvent front. In order to optimally fill the sugar pocket, the partially solvent-exposed tetrahydropyranyl moiety adopts a roughly orthogonal orientation with respect to the scaffold.¹⁴⁸

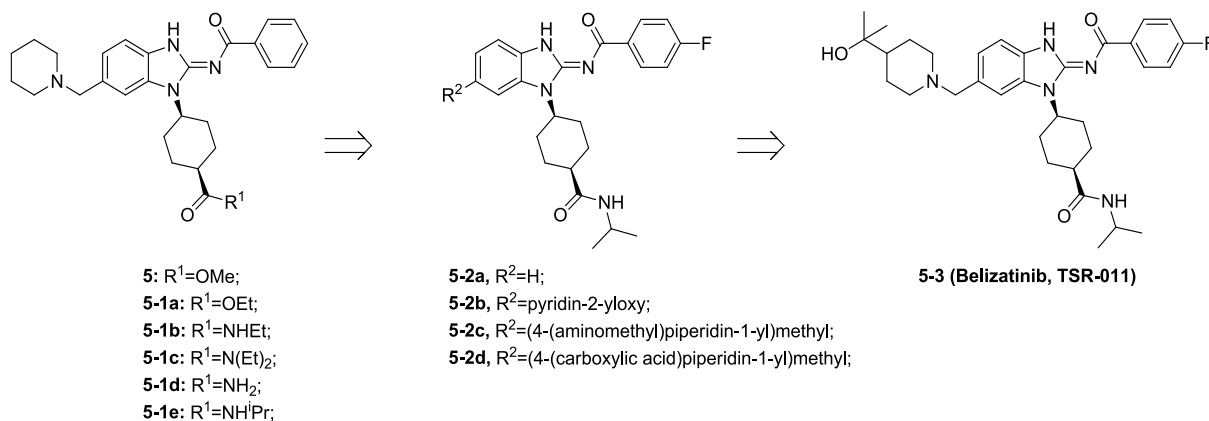


Figure 9. Structural optimization from compound **5** to **5-3**.

Another drug discovery campaign centered on ALK serendipitously uncovered **5-3 (Belizatinib, TSR-011)**, a novel, potent TRK inhibitor (Figure 9).¹⁵² Through HTS (high-throughput screening), Lewis *et al.* identified the ALK inhibitor **5** (ALK kinase IC₅₀ = 0.003 μM, pALK cell IC₅₀ = 0.054 μM; 64-fold, 103-fold, 15-fold selectivity over JAK2, SRC, and IGF1R, respectively),¹⁵² which was co-crystallized with ALK (Figure 10A).¹⁵² Through the benzoyl carbonyl oxygen and the benzimidazole NH, **5** was shown to bind to the hinge of ALK at Met1199 and the benzoyl ring was adjacent to the gatekeeper residue Leu1196. The *cis*-1,4 geometry of the cyclohexyl group pushes the methyl ester moiety into a hydrophobic pocket surrounded by Leu1256 and Gly1269. The piperidine moiety engages in Van der Waals interactions with two backbone carbonyls on the N-terminal lobe (Gly1121, Leu1122) in a shallow pocket on the surface of the protein at the entrance to the ATP binding pocket.¹⁵²

To improve cell potency, selectivity, and metabolic stability, SAR optimization was completed. First, the methyl ester was replaced with different esters and amides (compounds **5-1a** to **5-1e**). The isopropyl amide compound **5-1e** displayed the best combination of activity and selectivity (ALK kinase IC₅₀ = 0.002 μM, pALK cell IC₅₀ = 0.054 μM; 813-fold, 429-fold, 36-fold selectivity over JAK2, SRC, and IGF1R, respectively).¹⁵² To improve metabolic stability, a wide variety of modifications were investigated at the R² position. Figure 9 depicts some of these modifications, and the tertiary alcohol analogue **5-3** appeared optimal. Finally, different substitutions were introduced to the 4-fluoro phenyl ring; however, these derivatives either decreased selectivity or suffered from compromised cellular activity against

ALK.¹⁵² When screening **5-3** against a kinase panel, **5-3** was found to have potent pan-TRK activity (IC_{50} for TRKA/B/C < 0.003 μ M).¹⁵³ Currently, **5-3** is under a Phase 1/2 study in patients with advanced solid tumors and lymphomas. (NCT02048488).

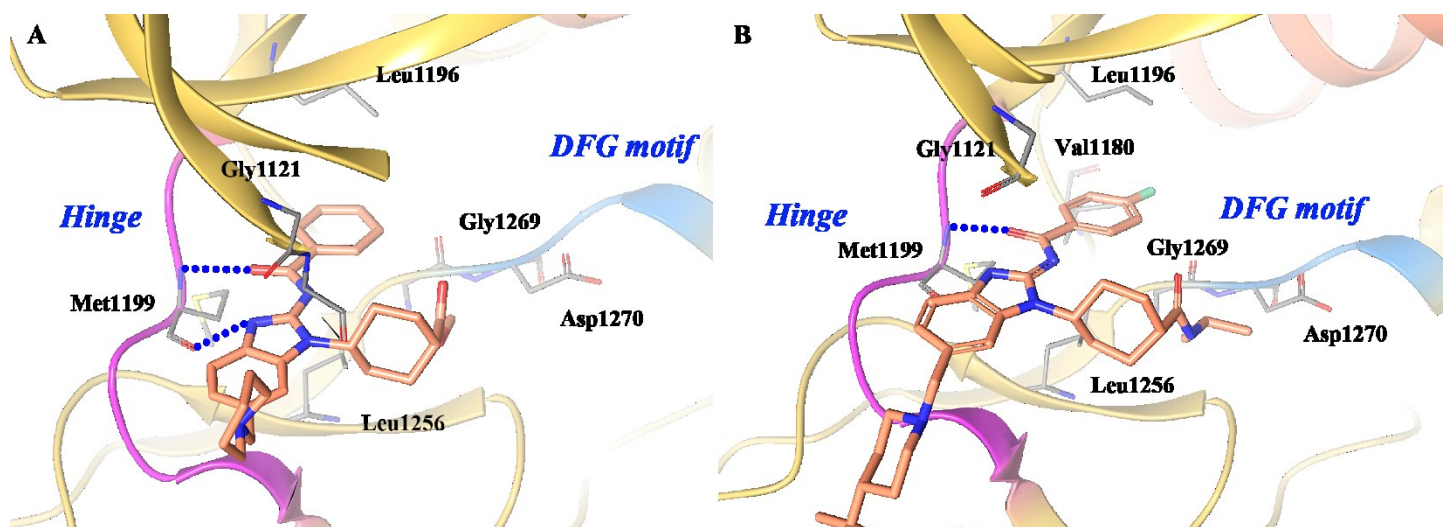


Figure 10. (A) Co-crystal structure of compound **5** in ALK (PDB ID: 4FOC, 1.7 Å); (B) Co-crystal structure of compound **5-3** in ALK (PDB ID: 4FOD, 2 Å). The kinase is depicted in yellow ribbons, and the hydrogen bonds are illustrated in blue dashed lines.

The co-crystal structure of **5-3** with ALK (Figure 10B) shows that **5-3** binds similar to **5** (Figure 10A).¹⁵² Compound **5-3** pushes into the active site of the kinase in a pocket formed by Val1180 and Leu1256, and is in close proximity to the gatekeeper residue Leu1196. The iminobenzamide moiety adopts the exocyclic acylimine tautomer permitting key hydrogen bonding interactions with the hinge region residue Met1199. This tautomer is favored by extended π -delocalization into the pendant aryl ring, achieved by retaining a coplanar arrangement between benzamide and benzimidazole moieties.¹⁵²

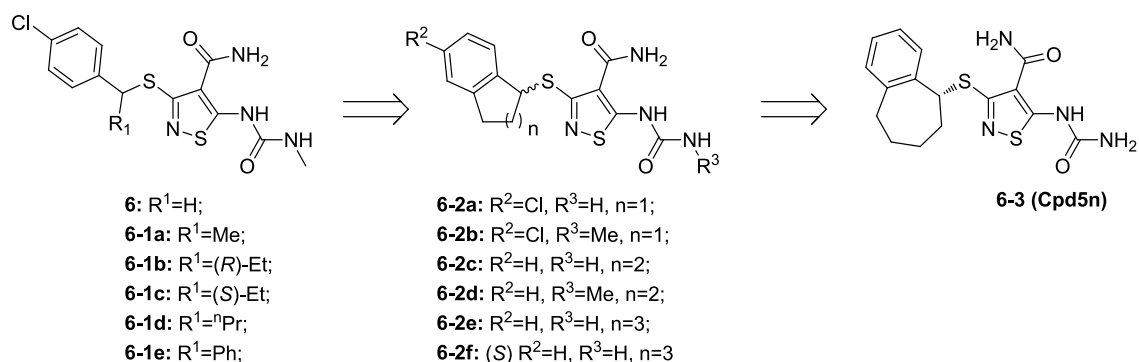


Figure 11. Structural optimization from compound **6** to **6-3**.

Isothiazole derivatives have been identified as TRK inhibitors (Figure 11). From an HTS campaign directed at TRKA, Lippa *et al.* identified compound **6** (TRKA IC₅₀= 0.007 μM).¹⁵⁴ Initial SAR studies at R¹ determined that substitution at the benzylic α-position remarkably influenced TKRA activity and VEGFR2 selectivity. Small aliphatic chains were well tolerated (**6-1a**, **6-1b**, TRKA IC₅₀s were 0.003 μM and 0.004 μM, respectively), while larger substitutions significantly diminished activity (**6-1d**, **6-1e**, TRKA IC₅₀s were 0.035 μM and 2.6 μM, respectively).¹⁵⁴ The orientation of the R¹ substitution also played a key role: the (*R*)-ethyl enantiomer **6-1b** was >10-fold more active (TRKA IC₅₀, 0.004 μM vs 0.052 μM) and was >100-fold more selective (VEGFR2 selectivity, 1,300X vs 10X) than the (*S*)-enantiomer. SAR at R² and R³ showed that substitution at these two positions are not necessary to maintain TRK activity (**6-2a to 6-2d**, TRKA IC₅₀s were 0.01 μM, 0.008 μM, 0.105 μM and 0.111 μM, respectively).¹⁵⁴ Further optimization identified that bicyclic moieties were important for TRK activity, especially the 7-membered ring system (compound **6-2e**, TRKA IC₅₀< 0.001 μM) and, consistent with previous data, the (*R*)-enantiomer was more active (**6-3** vs **6-2f**, TRKA IC₅₀s were <0.001 μM vs 0.091 μM). Compound **6-3 (Cpd5n)** had pico-molar kinase potency and single-digit nanomolar activity against TRK-driven cell growth.¹⁵⁴

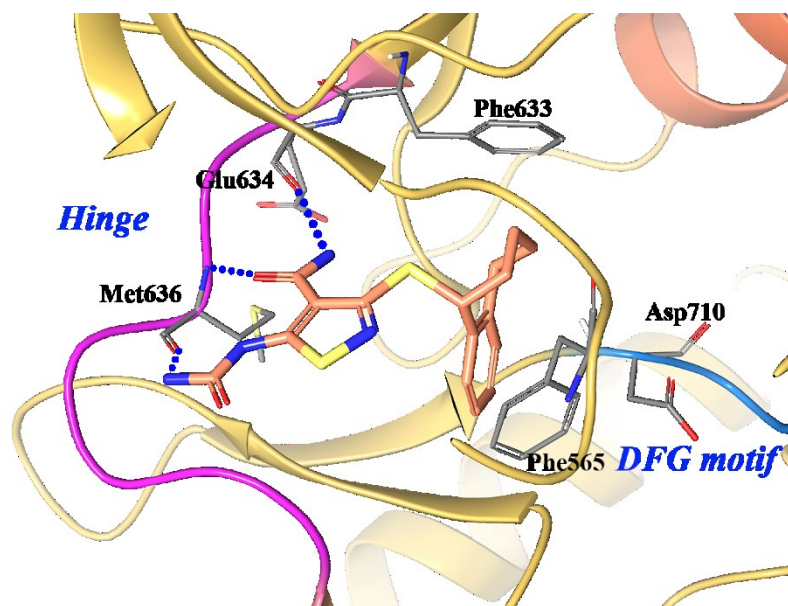


Figure 12. Co-crystal structure of compound **6-3** in TRKB (PDB ID: 4AT3, 1.77 Å). The kinase is depicted in yellow ribbons, and the hydrogen bonds are illustrated in blue dashed lines.

The co-crystal complex of **6-3** in TRKB was obtained and is shown in Figure 12.⁷³ The aliphatic portion of **6-3** is oriented towards the glycine-rich loop and exhibits clear, Type I binding.⁷³ The glycine-rich loop forms a cage around the inhibitor and engages in strong, hydrophobic interactions through Phe565. The urea and amide groups on the thiazole bind to the hinge of TRKB, forming three hydrogen bonds. The benzo-cycloheptene group is sandwiched between the gatekeeper Phe633 and glycine-rich loop Phe565 side chains, likely contributing to the stabilization of the TRKB DFG-in conformation.⁷³ This also explains the potency differences between the two enantiomers as the *S*-enantiomer could still bind the hinge but would clash with Phe565 due to difference in stereochemistry of the benzo-cycloheptene. The affinity of **6-3** for TRKB is also enhanced by several water-bridged hydrogen bonds between the inhibitor and the kinase.⁷³

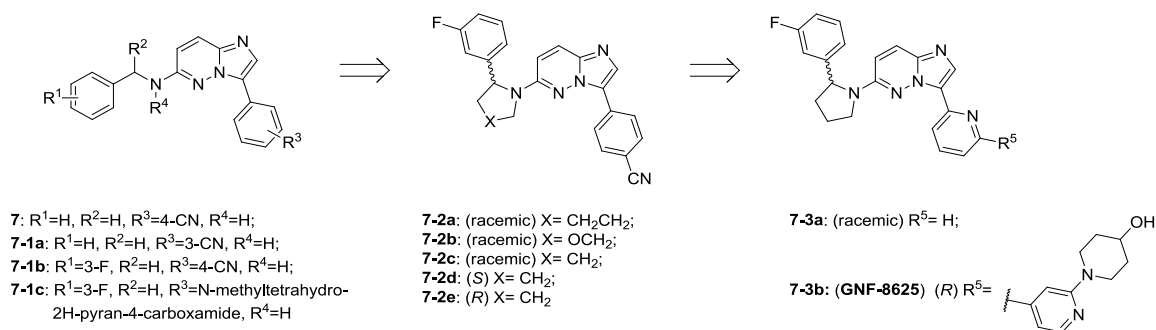


Figure 13. Structural optimization from compound **7** to **7-3b**.

In another campaign to uncover novel TRK inhibitors, Choi *et al.* developed a series of substituted imidazopyridazine derivatives from compound **7** (TRKB IC_{50} = 0.083 μ M) (Figure 13).¹⁵⁵ The crystal complex of **7** with TRKC (Figure 14A) shows that the ligand binds to the inactivated (DFG-out) form of the kinase and the imidazopyridazine warhead engages in a hydrogen bond at the hinge with Met620. The benzonitrile ring is wedged between Phe617 and Phe698, and the phenyl ring sits under the glycine-rich loop and faces the solvent front of the active site.¹⁵⁵

Preliminary medicinal chemistry efforts focused SAR studies at R^1 to R^4 , with the goal of identifying compounds with improved potency and pharmacokinetic properties suitable for *in vivo* profiling. Nitrile substitutions in the phenyl group (R^3) at the 3- or 4-position were equally tolerated (**7** vs **7-1a**, TRKA cell IC_{50} s = 0.85 μ M and 0.74 μ M). It was also observed that 3-substitution at the benzylamine phenyl ring (R^1) led to a 10-fold increase in potency (**7-1b**, TRKA cell IC_{50} = 0.076 μ M).¹⁵⁵ Modifying the phenyl ring (R^3) with 3-F substitution at R^1 furnished many tolerated functional groups that could either increase solubility or further drive potency (i.e. compound **7-1c**, TRKA cell IC_{50} = 0.006 μ M). Methylation of the benzylic amine (R^3) led to no significant change in potency indicating that the acidic proton on the benzylic amine does not hydrogen bond with TRK.¹⁵⁵ Cyclizing the benzyl amine moiety with the adjacent phenyl ring was performed to rigidify the structure and reduce conformational entropy. The fused, five-membered ring system was optimal for TRK inhibition and exhibited a preference for the *R*-enantiomer (**7-2a** to **7-2e**, TRKA cell IC_{50} s = 0.17 μ M, 0.075 μ M, 0.068 μ M, 3.13 μ M, and 0.021 μ M, respectively). Derivatization at R^5 led to the discovery of the optimized compound **7-3b** (**GNF-8625**).¹⁵⁵ Compound **7-3b** demonstrated potent, antiproliferative activity against TRK transfected Ba/F3 and KM-12 cell lines (IC_{50} = 0.001 μ M and 0.01 μ M, respectively). In a KM-12-derived tumor xenograft, compound **7-3b** demonstrated antitumor efficacy in a dose dependent manner, inducing 20% tumor regression at a dose of 50 mg/kg BID.¹⁵⁵

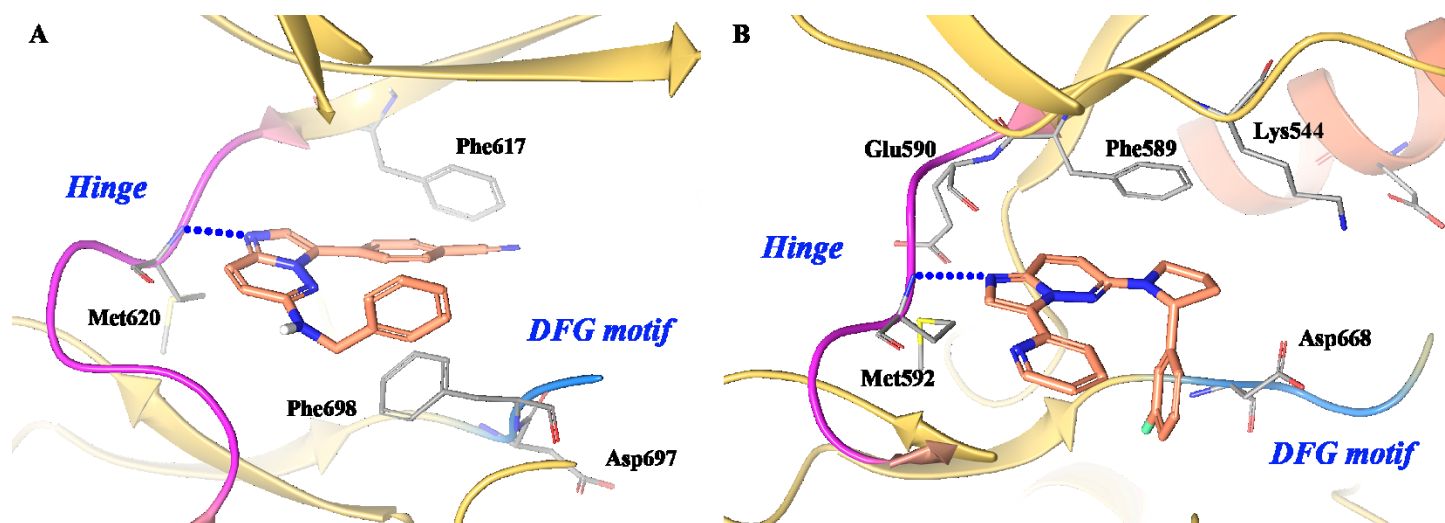


Figure 14. (A) Co-crystal structure of compound **7** in TRKC (PDB ID: 4YMJ, 2 Å); (B) Co-crystal structure of compound **7-3a** in TRKA (PDB ID: 4YNE, 2.02 Å). The kinase is depicted in yellow ribbons, and the hydrogen bonds are illustrated in blue dashed lines.

Imidazopyridazines are frequently incorporated into kinase inhibitors as they readily form a hydrogen bond at the hinge with the C-6 carbon oriented towards the solvent.¹⁵⁶ The warhead of **7-3a** is based on imidazopyridazine and was expected to bind TRKA akin to **7**. Surprisingly, the co-crystal structure of **7-3a** with TRKA revealed an unexpected 180° rotation of the imidazopyridazine core at the hinge (Figure 14B).¹⁵⁵ Only the (*R*)-enantiomer of **7-3a** is active because the 3-F-phenyl is optimally positioned downwards in the hydrophobic pocket. The moiety fills a pocket endogenously occupied by Phe669 and provides excellent shape complementary, likely contributing to increased affinity. Molecular modeling and crystallography studies indicated that two distinct binding modes exist (i.e. core flipping) with scaffold **7**.¹⁵⁵ Based on the different TRK co-crystal structures obtained with **7** and **7-3a**, it was concluded that the preferred binding mode depends on C-6 substitution. If the C-6 substitution is modified to (*R*)-phenylpyrrolidine, the “flipped” orientation is preferred as the pyrrolidine anchors the phenyl group in the hydrophobic pocket.¹⁵⁵ The phenomenon of ‘core flipping’ could be employed to generate compounds with activity in multiple kinase families. Based on the crystal structure, compound **7-3a** is a Type I kinase inhibitor.

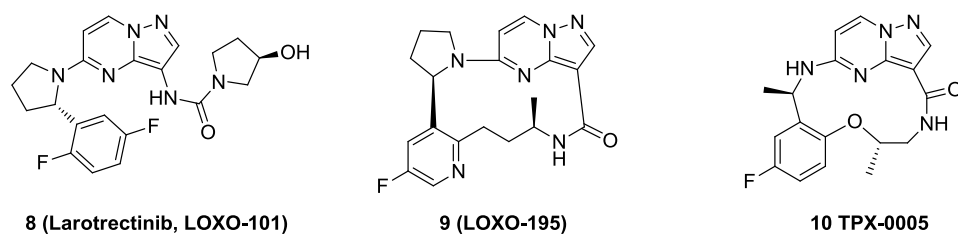


Figure 15. Chemical structures of compound **8**, and second generation TRK inhibitors **9** and **10**.

Compound **8** (**Larotrectinib**, **LOXO-101**) is another selective, pan-TRK inhibitor exhibiting low nanomolar cellular potency against the TRK family (IC_{50} ranging from 0.002 μ M to 0.02 μ M) with 100-fold selectivity over other kinases (Figure 15).^{49, 157} The compound can induce cell-cycle arrest in the G1 phase and apoptosis in KM-12 cells.⁴⁹ Compound **8** is currently in a Phase 2, open-label study for patients with advanced solid tumors harboring a fusion of TRKA, TRKB, or TRKC (NCT02576431).⁴⁸ The medicinal chemistry effort leading to the discovery of this compound and its co-crystal complex with TRK have not been reported. However, because of the structure similarities between compounds **8** and **7-3b**, it can be inferred that **8** exhibits similar SAR properties to that of **7-3b**.

Second Generation Type I TRK Inhibitors

All first generation TRK inhibitors exhibit profound, upfront efficacy but eventually lose effectiveness due to the development of secondary mutations in the TRK kinase domain. After treatment with **8** or **4-3** mutations in the TRK kinase domain have been reported,¹⁵⁸ which renders further treatment ineffective.^{47, 159} These mutations include TRKA^{G595R} (and its paralogue TRKC^{G623R}) in the solvent front of the active site, TRKA^{G667C} (and its paralogue TRKC^{G696A}) adjacent to the DFG motif, and TRKA^{F589L} at the gatekeeper region.^{47, 99, 159-161} TRKA^{G595R} and TRKA^{G667C} are analogous to ALK^{G1202R} and ALK^{G1269A}, respectively.¹⁵⁹ In TRKA, the native residues are important to accommodate **8** and **4-3**, while the mutations create steric clashes with the inhibitors. In addition, TRKA^{G595R} increases ATP affinity to the kinase.¹⁵⁹ Structural modeling suggests that each mutation directly interferes with binding of **8**, **4-3**, and all other TRK tyrosine kinase inhibitors.^{47, 160} Functional studies have subsequently confirmed that cancer cells harboring these mutations are cross-resistant to all TKIs with anti-TRK activity.¹⁶²⁻¹⁶³

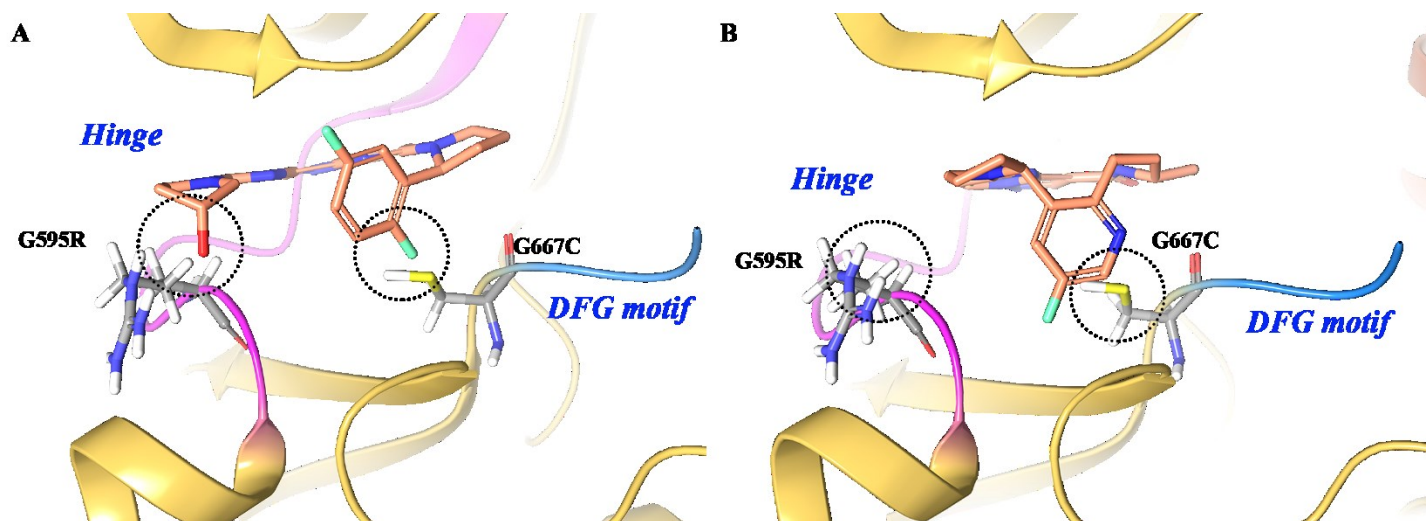


Figure 16. (A) Proposed binding and steric interactions of **8** with the TRKA double mutant G595R and G667C, (B) Proposed binding of **9** to the TRKA double mutant; steric interactions are not predicted between G595R and G667C. The kinase is depicted in yellow ribbons.¹⁶⁴

To generate inhibitors that could overcome point mutations in TRK, compounds **9** (LOXO-195) and **24** (TPX-0005) were designed to limit the compound surface area in the active site. (Figure 16). Both compounds were designed as fused macrocycles to reduce unnecessary interactions at either end of the binding pocket. Modelling suggested that TRKA^{G595R} would introduce steric clashes between the arginine side chain and the hydroxypyrrolidine group of **8**, and TRKA^{G667C} would create steric clashes between the cysteine or alanine side chain and the difluorophenyl group of **8** (Figure E).¹⁵⁹ To determine the impact of TRK kinase mutations on inhibitor activity, **8** and **9** were tested against TRKA^{G595R}, TRKA^{G667C}, and TRKC^{G623R}. Compound **9** achieved low nanomolar inhibitory activity against all mutated kinase (IC₅₀s = 0.002 μ M, 0.00098 μ M, and 0.0023 μ M); while compound **8** displayed significantly reduced inhibitory activity (IC₅₀s = 0.069 μ M, 0.045 μ M, and 0.048 μ M).¹⁵⁹ An innovative first-in-human clinical trial has demonstrated efficacy of compound **9** in 2 patients who had developed acquired resistance to **8** mediated by secondary TRKA^{G595R} or TRKA^{G623R} mutations.¹⁵⁹ Compound **10**, an analogue to **9**, potently inhibited ROS1^{G2032R} (IC₅₀ = 0.0084 μ M), TRKA^{G595R} (IC₅₀ = 0.0004 μ M), TRKB^{G639R} (IC₅₀ = 0.0019 μ M) and TRKC^{G623R} (IC₅₀ = 0.0004 μ M).¹⁶⁵ **10** also exhibited activity in xenograft tumor models bearing WT and kinase domain mutations of ALK, ROS1 and TRKA.¹⁶⁵⁻¹⁶⁶

Other Type I TRK Inhibitors

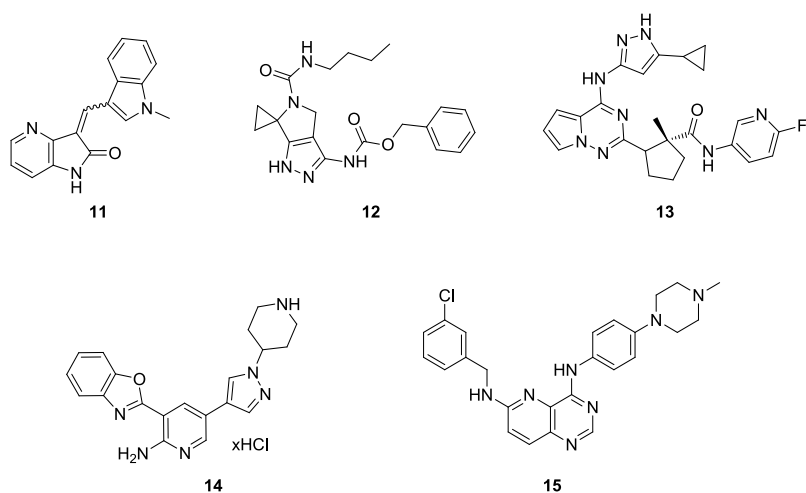


Figure 17. Chemical structures of other Type I TRK inhibitors

Several other TRK scaffolds have been reported that exhibit Type I characteristics and are summarized in the following section (Figure 17). Aza-oxindole and oxindoles were reported as potent TRK inhibitors by Wood *et al.*¹⁶⁷ The representative compound **11** exhibited pan-TRKA inhibitory activity (TRKA/B/C IC_{50} s = 0.030 μ M, 0.007 μ M, 0.005 μ M, respectively) with selectivity in the greater kinome but also inhibited VEGFR2 (vascular endothelial growth factor receptor 2).¹⁶⁷⁻¹⁶⁸ Compound **11** shares similarities in structure to other known VEGFR2 inhibitors, such as sunitinib, which likely accounts for its VEGFR2 profile.¹⁶⁷ Choe *et al.* reported a series of pyrrole[3,4-*c*]pyrazole TRKA inhibitors (Figure 17). The representative compound **12** inhibits TRKA with an IC_{50} of 0.019 μ M. SAR studies indicated that the cyclopropyl and benzyl carbamate groups are essential for potency and removal of either resulted in a loss of activity.¹⁶⁹ Carboni *et al.* developed compound **13** as a dual IGF-1R/IR inhibitor (IC_{50} = 0.0018 μ M and 0.0017 μ M, respectively). Kinase profiling showed that compound **13** was active on several other kinases, including TRKA/B (IC_{50} s = 0.007 μ M and 0.004 μ M, respectively).¹⁷⁰ Cho *et al.* developed compound **14** as a c-MET inhibitor based on an aminopyridine core substituted with benzoxazole (IC_{50} = 0.08 μ M).¹⁷¹ Compound **14** was later identified to have activity against the mutant c-MET^{Y1230D} kinase (IC_{50} = 0.003 μ M) and TRKA (IC_{50} = 0.039 μ M).¹⁷² Stachel *et al.* reported a series of pyrido[3,2-*d*]pyrimidine as TRKA inhibitors; the representative compound **15** had a TRKA IC_{50} of 0.011 μ M and moderate cell activity (IC_{50} =1.688 μ M).¹⁷³

Radiolabeled Type I TRK Inhibitors

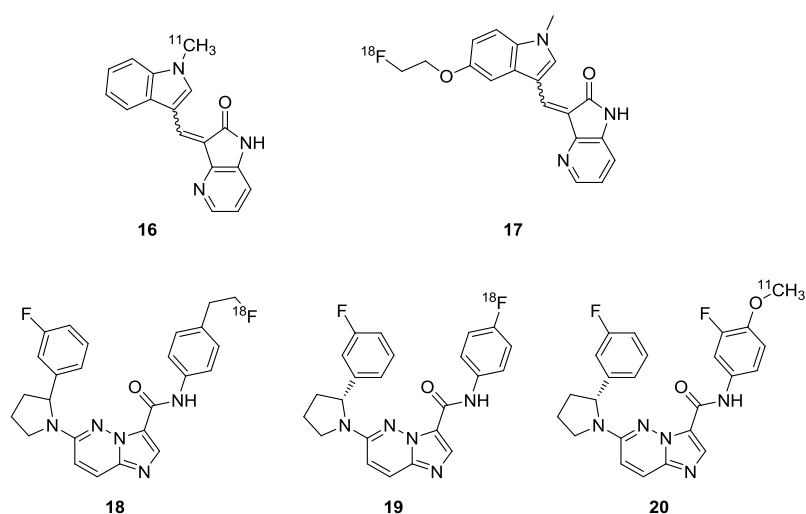


Figure 18. Chemical structures of representative radiolabeled Type I TRK Inhibitors.

Positron emission tomography (PET) is a non-invasive *in vivo* imaging technique that enables the visualization and quantification of the distribution of molecules labeled with positron-emitting isotopes. This method enables the evaluation of biochemical and physiological processes by monitoring the distribution and kinetics of a labeled molecule *in vivo*, and has found broad application in clinical practice (personalized treatments), research, and pharmaceutical development.¹⁷⁴⁻¹⁷⁷

Because of the clinical importance of TRK in cancer as well as the central nervous system, Bernard-Gauthier *et al* generated radiolabeled TRK ligands to assess and monitor TRKA/B/C levels in the brain. The TRK ligands were synthesized from known inhibitors using ¹¹C- or ¹⁸F-labeled PET radiotracers suitable for *in vivo* imaging (compounds **16-20**) (Figure 18).^{168, 178-182} These compounds demonstrated comparable activity and selectivity profiles to the unlabeled precursor.¹⁸⁰ Compound **16** displayed excellent TRK selectivity in a panel of brain and cancer relevant kinases and TRK-specific binding *in vitro* in rat brain and human neuroblastoma cryosections. The radio-compound also exhibited uniform regional brain distribution but was highly susceptible to CYP450 metabolism.¹⁶⁸ Nevertheless, TRK radio-compounds can prove instrumental in studying TRK biology, diagnosing TRK-positive disease, and determining drug disposition of TRK inhibitors in real time.^{175, 177} It is worth noting that compound **19** was the first TRK radiotracer clinical lead involved in a non-human primate imaging study;¹⁸² compound **20** was the first reported radiotracer used as an *in vivo* probe to explore endogenous kinase densities using PET neuroimaging in humans.¹⁸¹

Type II TRK Inhibitors

Type I TRK inhibitors are ATP competitive and typically possess pan-kinase activity. A method to increase kinase selectivity and potency is to generate inhibitors that bind in a Type II fashion.¹⁸³ Type II inhibitors are generally more active against tyrosine kinases, which can be exploited to increase selectivity and potency profiles.¹⁸⁴ TRK inhibitors that display Type II binding kinetics can be preferred depending on the biology being studied or the disease being treated. It is important to note that the most advanced TRK inhibitors in clinical trials are Type I (**8** and **4-3**). These inhibitors are being evaluated for anticancer properties and may have inhibition characteristics optimal for a tumor environment. In other therapeutic areas, such as the central nervous system (CNS) or pain management, TRK inhibitors with a Type II profile may be preferred because, as a class, they are more selective than Type I inhibitors.¹⁸⁴ However, the typically larger molecular architecture of Type II compounds can cause less favorable drug-like properties, leading to development challenges. In the following section, the development of Type II TRK inhibitors is disclosed, and developmental efforts were primarily focused on optimizing for anticancer properties.

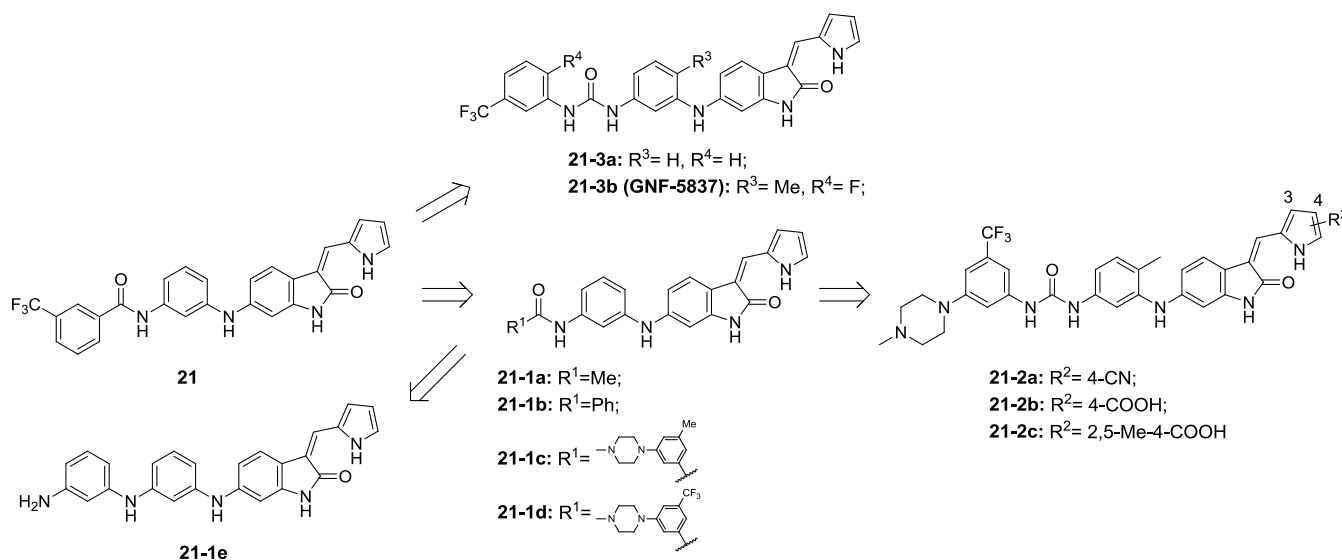


Figure 19. Structural optimization from compound **21** to **21-3b (GNF-5837)**.

Albaugh *et al* identified Type II TRK inhibitors based on an oxindole-core (Figure 19).¹⁸⁵ Oxindole **21** inhibited Ba/F3-Tel-TRKA/B/C with IC_{50} s less than 0.06 μM . SAR studies at the R^1 position showed that the phenyl ring is critical for TRK specific inhibitory activity (**21-1a** vs **21-1b**, TRKA cell IC_{50} : 2.3 μM vs 0.91 μM).¹⁸⁵ To improve drug properties,

several basic groups were introduced at the terminal phenyl ring and were well tolerated and increased potency, but did not improve solubility. Substituting the aryl ring with 3-CF₃ at R¹ is crucial for TRK activity (**21-1c** and **21-1d**, TRKA cell IC₅₀: 0.39 μ M and 0.013 μ M 0.39 μ M, respectively). Truncating the amide group to aniline resulted in a total loss of activity, indicating the amide is necessary for TRK activity (**21-1e**, TRKA cell IC₅₀ > 10 μ M).¹⁸⁵ Replacement of the pyrrole with other groups or methylation of the pyrrole nitrogen yielded significantly less potent compounds suggesting that the acidic proton on pyrrole is involved in a key hydrogen bond at the hinge region. Substitution on the pyrrole showed that carboxylic acid at position 4 is preferred for potency and selectivity, with or without methyl substitution (**21-2a** to **21-2c**, TRKA cell IC₅₀: 0.014 μ M, 0.01 μ M, and 0.012 μ M; selectivity: 43-fold, 150-fold and 108-fold, respectively).¹⁸⁵ Replacement of the amide with urea generated compounds with increased potency and selectivity over VEGFR2 (**21-3a**, TRKA cell IC₅₀ = 0.004 μ M, selectivity 130-fold).¹⁸⁵ Introduction of a methyl substitution at R³ and a fluorine at R⁴ generated compound **21-3b** (GNF-5837), which exhibits pan-TRK inhibition (TRKA/B/C IC₅₀s = 0.011 μ M, 0.009 μ M, 0.007 μ M, respectively) and about 300-fold selectivity over VEGFR2 (IC₅₀ = 3.0 μ M). In BALB/c mice and Sprague–Dawley rats, compound **21-3b** demonstrated low drug clearance and moderate bioavailability. In mice bearing RIE xenografts expressing TRKA and NGF, compound **21-3b** (100 mg/kg/d P.O.) significantly inhibited tumor growth.¹⁸⁵

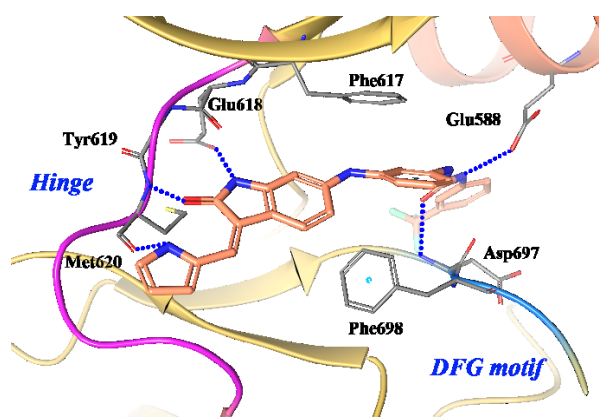


Figure 20. Co-crystal structure of compound **21-3a** in TRKC (PDB ID: 3V5Q, 2.2 Å). The kinase is depicted in yellow ribbons, and the hydrogen bonds are illustrated in blue dashed lines.

In the co-crystal structure of **21-3a** with TRKC (Figure 20), **21-3a** is found to bind to the kinase in a Type II manner.¹⁸⁵ The oxindole core and pyrrole nitrogen form key hydrogen bonds with hinge residues Glu618, Tyr619, and Met620. The urea functionality interacts with Glu588 from the α -C-helix and Asp697 from the DFG motif. In addition,

interactions occur at the phenyl bridge with Phe617 (gatekeeper) and a face to edge interaction with Phe698 from the DFG motif.¹⁸⁵

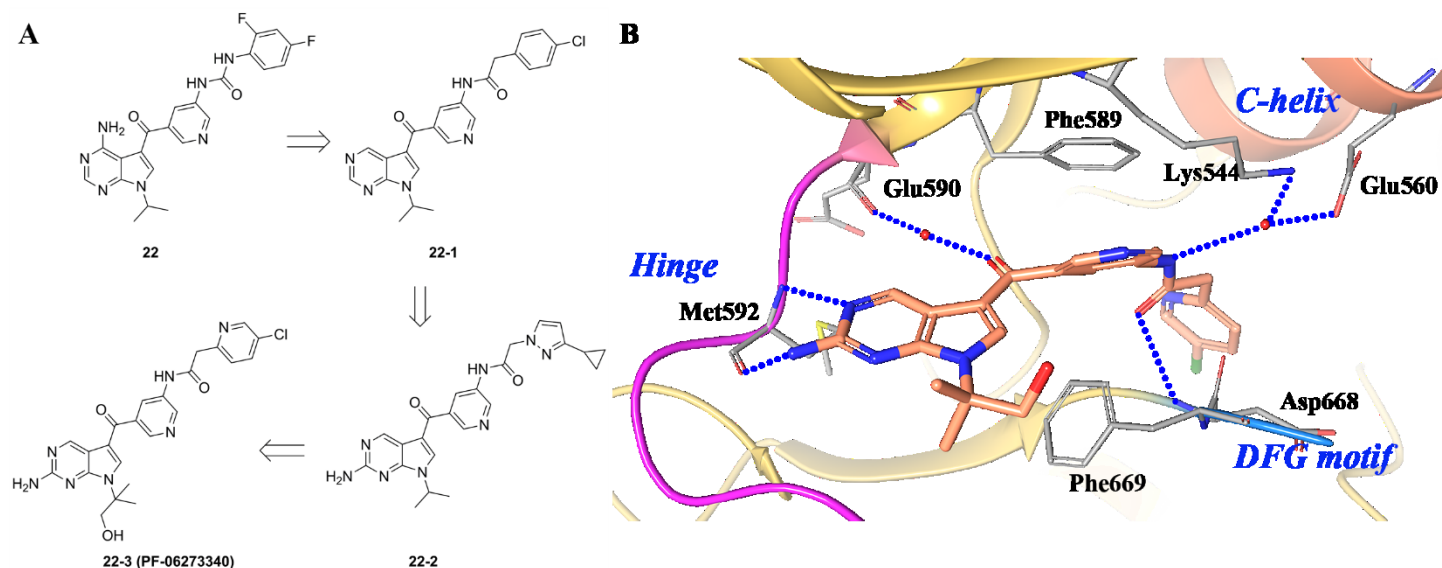


Figure 21. (A) Structural optimization from compound **22** to **22-3**; (B) Co-crystal structure of compound **22-3** with TRKA (PDB ID: 5JFX, 1.63 Å). The kinase is depicted in yellow ribbons, and the hydrogen bonds are illustrated in blue dashed lines.

Skerratt *et al.* reported a series of pyrrolopyrimidine derivatives as pan-TRK inhibitors (Figure 21A).¹⁸⁶ By employing a high-throughput TRKA/B cell screening assay, compound **22** was identified as a pan-TRK inhibitor (TRKA/B/C IC_{50} s = 0.002 μ M, 0.005 μ M, and 0.004 μ M, respectively) with strong kinome selectivity but poor water solubility (< 0.3 μ M).¹⁸⁶ To improve solubility, the urea group was replaced with an amide and the 4-NH₂ was removed to generate compound **22-1** (TRKA/B/C IC_{50} s = 0.012 μ M, 0.004 μ M, and 0.003 μ M, respectively) with improved water solubility (~13.2 μ M).¹⁸⁶ It was determined that the scaffold was likely metabolized by aldehyde oxidase and inhibited hERG (human Ether-à-go-go-Related Gene) potassium heart channels.¹⁸⁷⁻¹⁸⁸ In order to reduce metabolic liabilities and off target toxicities, an amino group was added at the 2-position furnishing compound **22-2** (TRKA/B/C IC_{50} s = 0.008 μ M, 0.005 μ M, and 0.004 μ M, respectively; solubility = 30 μ M).¹⁸⁶ To further improve physical-chemical properties and aqueous solubility, a hydrophilic hydroxymethylene group was added to N-Pr motif and the terminal ring was replaced with pyridine to obtain compound **22-3** (PF-06273340). Compound **22-3** was a potent pan-TRK inhibitor (TRKA/B/C

IC_{50} s = 0.006 μ M, 0.004 μ M, and 0.003 μ M, respectively; solubility= 131 μ M) and exhibited selectivity over a large kinase panel.¹⁸⁶ Currently, Phase 1 clinical trials are ongoing to examine the activity of different doses of **22-3** on a panel of evoked pain tests in healthy male subjects (NCT02260947).

Figure 21B shows the co-crystal structure of **22-3** bound to TRKA and highlights key protein–ligand interactions.¹⁸⁶ Compound **22-3** binds to the DFG-out form of TRK, with the 2-aminopyrrolopyrimidine forming hydrogen bonds at the hinge and the ketone binding to Glu590 through a water contact.¹⁸⁶ Most kinase inhibitors engage in one or two interactions at the hinge, while **22-3** is found to engage in three. The central pyridine group of **22-3** engages in a double π - π stacking interaction with Phe589 (gatekeeper residue) and Phe669 (DFG motif). The carbonyl oxygen forms a hydrogen bond with the amide backbone of Asp668 (DFG motif) and the amide engages TRKA through a water contact between Lys544 and Glu560 from the c-Helix. The lipophilic back pocket accommodates the chloropyridine group.¹⁸⁶ Based on the binding characteristics of **22-3**, the inhibitor can be considered Type II.

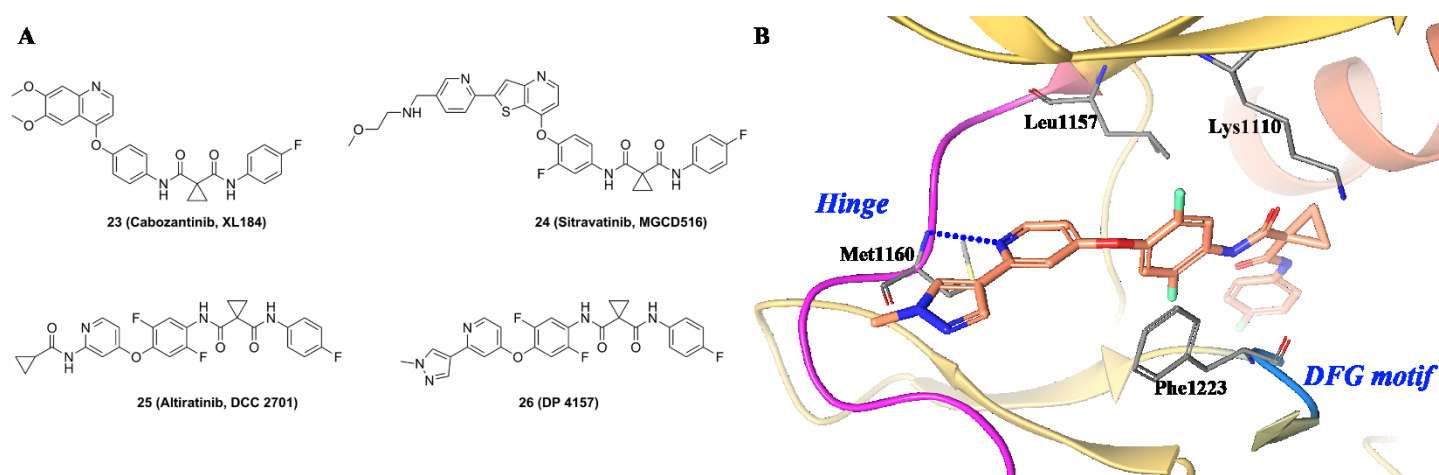


Figure 22. (A) Chemical structures of representative dicarboxamide TRKA inhibitors; (B) Co-crystal structure of compound **26** in c-MET (PDB ID: 5DG5, 2.6 Å). The kinase is depicted in yellow ribbons, and the hydrogen bonds are illustrated in blue dashed lines.

Compound **23** (Cabozantinib, XL184) is a multiple kinase inhibitor with activity against c-MET/VEGFR2 and was found to have a potent TRKB inhibitory activity ($IC_{50} < 0.02$ μ M) (Figure 22A).¹⁸⁹ Compound **23** is currently under Phase 2 clinical trials in patients with RET fusion-gene non-small cell lung cancer and those with other activating genes,

such as ROS1, NTRK, MET or AXL (NCT01639508). Compound **24** (**Sitravatinib**, **MGCD516**) was developed by Patwardhan *et al.* as a potent multi-kinase inhibitor (Figure 22A) active against several kinases (IC₅₀s for AXL: 0.0015 μ M, VEGFR2: 0.005 μ M, FLT3: 0.008 μ M, c-KIT: 0.006 μ M, TRKA: 0.005 μ M, and TRKB: 0.009 μ M). Compound **24** blocked phosphorylation of several RTKs and induced potent anticancer effects *in vitro*; the compound was also active *in vivo* in MPNST (neurosarcoma) and LS141 (hybridoma) mouse xenograft models.¹⁹⁰ Compound **24** is currently under Phase 1 clinical development for patients with advanced solid tumor malignancies (NCT02219711). Compound **25** (**Altiratinib**, **DCC2701**) was reported by Smith *et al.* as a multi-targeted kinase inhibitor with preferential activity on MET, TIE-2, and VEGFR2 (IC₅₀s = 0.0027 μ M, 0.008 μ M, and 0.0092 μ M, respectively) (Figure 22A). Subsequently, **25** was identified to exhibit activity as a pan-TRK inhibitor (TRKA/B/C IC₅₀s = 0.00085 μ M, 0.0046 μ M, and 0.0083 μ M, respectively) and FLT3 inhibitor (IC₅₀ 0.0093 μ M).¹⁹¹ In cell antiproliferative assays, compound **25** exhibited IC₅₀s of 0.00069 μ M in K562 cells, 0.0012 μ M in SK-N-SH cells, and 0.0014 μ M in KM-12 cells. Compound **25** inhibited tumor growth in the MET-amplified MKN-45 xenograft model in a dose-dependent manner. Further, compound **25** can actively penetrate the blood-brain-barrier, indicating its potential for the treatment of brain cancers, brain metastases, and cancer pain. Compound **25** is currently under Phase 1 clinical development for patients with advanced solid tumors with NTRK or MET genomic alterations (NCT02228811).

Figure 22B illustrates the general Type II binding mode of the dicarboxamide kinase inhibitor class.¹⁹¹ The pyridine of **26** (**DP4157**) binds to the hinge region and forms a hydrogen bond with Met1160. The central di-fluoro phenyl ring is in a hydrophobic pocket formed by Lys1110, Leu1157 and Phe1223, and engages in a π - π stacking interaction with Phe1223. The terminal para-fluoro phenyl ring binds in the allosteric pocket between the DFG motif and α -C-helix.¹⁹¹

Other Type II TRK Inhibitors

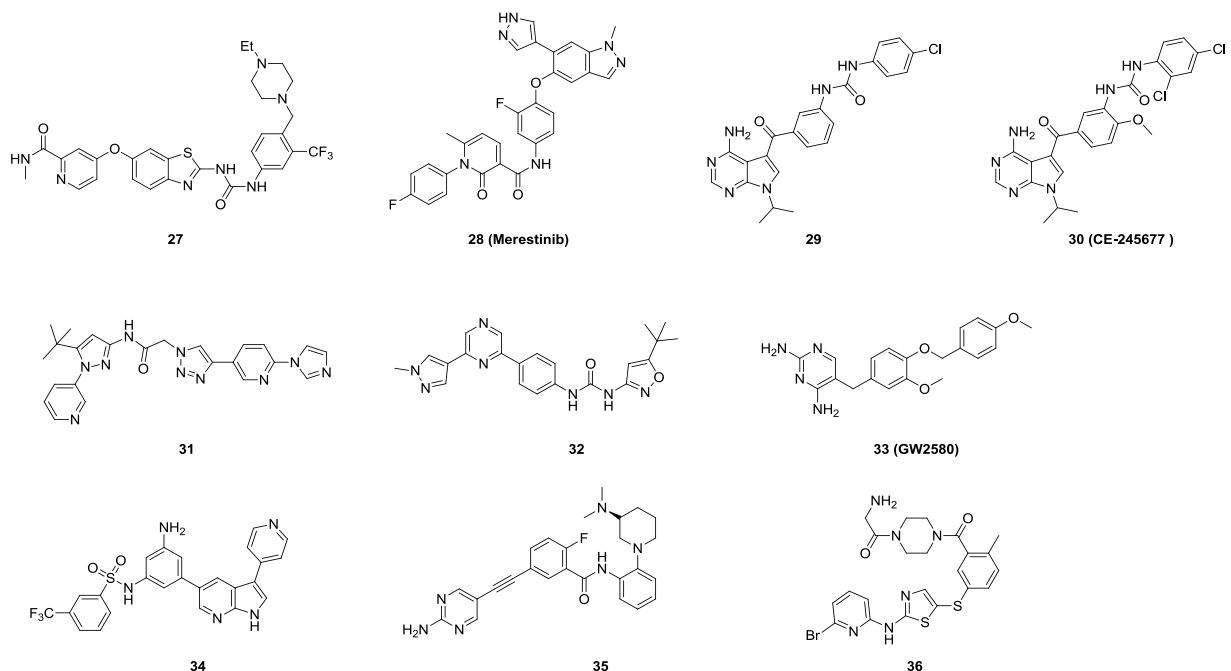


Figure 23. Chemical structures of other Type II TRK inhibitors

El-Damasy *et al.* reported benzothiazole derivative **27** as multi-targeted kinase inhibitors (Figure 23).¹⁹² Compound **27** was active on several kinases with IC_{50} values below 0.1 μM (including VEGFR2, ABL, TRKA, TRKB, and TIE2 *et al.*). Specifically, the IC_{50} s for TRKA and TRKB were 0.0038 μM and 0.0044 μM , respectively. In antiproliferative studies, compound **27** was active against the KM-12 cell line with an IC_{50} of 0.019 μM . Arcari *et al.* reported a series of 4-aminopyrrolopyrimidine derivatives as TIE-2 inhibitors.¹⁹³ Compound **28** (Figure 23) was identified as a potent, pan kinase inhibitor with activity against c-MET (IC_{50} = 0.0047 μM) and RON (IC_{50} = 0.0012 μM) and exhibited anti-tumor activities in multiple mouse xenograft models.¹⁵⁷ Medicinal chemistry efforts led to the identification of compound **29** (Figure 23), which was found to be a TIE-2/TRKA dual inhibitor (IC_{50} for TIE-2 and TRKA were 0.0037 μM and 0.004 μM , respectively).¹⁹³ A close analogue of **29**, compound **30**, progressed to clinical trials, but the Phase I multiple dose trials were terminated due to the development of significant CNS adverse events, including cognitive deficits, personality changes, and sleep disturbances.^{28, 186} Compound **31** (Figure 23) is another compound reported by Stachel *et al.*¹⁷³ with good TRK inhibitory activity (TRKA IC_{50} = 0.009 μM , cell IC_{50} = 0.007 μM). This compound was found to bind to the TRK kinase in the DFG-out conformation.¹⁹⁴ On compound **31**, the imidazole warhead binds to the hinge region, the central triazole ring forms an interaction with the gatekeeper residue, and the pyrazole occupies a

selectivity pocket normally occupied by Phe669. This inhibitor is very unique because of the innovative triazole linker and imidazole warhead. Frett *et al* described pyrazine-based derivatives as TRKA inhibitors (Figure 23).¹⁹⁵ Compound **32** had a TRKA IC₅₀ of 0.005 μM (Figure 23), and modeling studies determined the compound binds in a typical Type II conformation. Compound **33** was initially reported by Conway *et al.* as a selective CSF-1R (colony stimulating factor 1 receptor) inhibitor (Figure 23), which completely inhibited CSF-1R *in vitro* at an IC₅₀ of 0.06 μM but was inactive against 26 other kinases.¹⁹⁶ Later, the same authors found compound **33** also inhibited TRKA with an IC₅₀ of 0.88 μM.¹⁹⁷ The radiolabeled analogue of **33** was reported by Bernard-Gauthier *et al.*¹⁸⁰ Bertrand *et al.* reported that compound **33** bound to TRKB in a DFG-out conformation.⁷³ Hong *et al.* reported a series of 3,5-disubstituted-7-azaindoles as TRK Inhibitors.¹⁹⁸ Further modification uncovered compound **34** (Figure 23), which is a pan-TRK inhibitor with selectivity over 30 kinases. The activity of compound **34** against TRK isoforms was equal (pan-TRK IC₅₀ = ~0.001 μM), but was 100-fold more selective against other kinases.¹⁹⁸ Amino pyrimidine derivatives were developed as TIE-2 (tunica interna endothelial-2) inhibitors with compound **35** (Figure 23) exhibiting TIE-2 inhibition (IC₅₀ = 0.005 μM) with almost equal TRKA inhibitory activity (IC₅₀ = 0.008 μM).¹⁹⁹ Through screening of an in-house kinase library, Kim *et al.* found 2-amino-5-(thioaryl)thiazole to be a promising scaffold for TRK inhibition.¹⁰⁸ Further SAR investigation led to the identification of compound **36** (Figure 23) (TRKA IC₅₀ = 0.0006 μM), which was selective over CDK, MET, and IGF-1R (IC₅₀s = 0.54 μM, >1 μM, and 0.43 μM, respectively).

Pseudo-Type II TRK Inhibitors

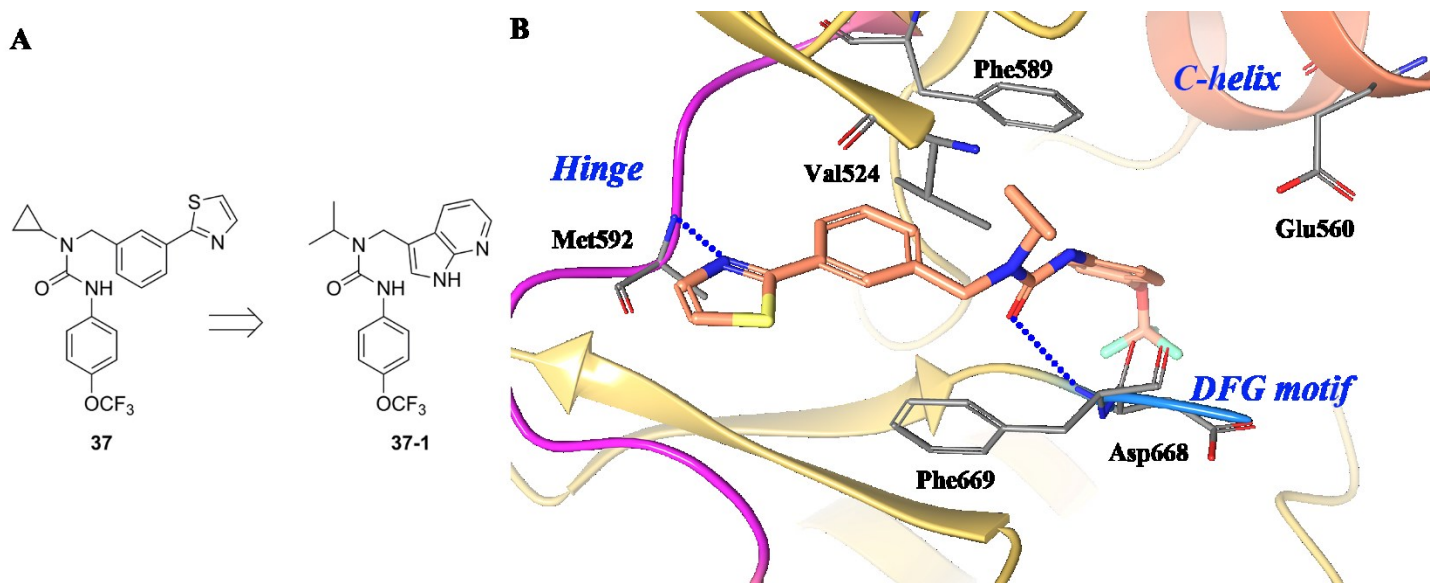


Figure 24. (A) Identification of compound **37-1**; (B) Co-crystal structure of compound **37** and its binding mode in TRKA (PDB ID: 4PMP, 1.8 Å). The kinase is depicted in yellow ribbons, and the hydrogen bonds are illustrated in blue dashed lines.

A quintessential property of Type II inhibitors is the formation of a strong hydrogen bond at the hinge region.¹³⁷ In certain inhibitors of TRK, however, the hydrogen bond at the hinge is abnormally weak with the majority of important interactions occurring in an adjacent allosteric pocket. This was first reported by Stachel *et al.* with the development of urea based compound **37** (Figure 24A) (TRKA kinase IC_{50} = 4.233 μ M, cell IC_{50} = 0.549 μ M).¹⁷³ Structure optimization resulted in the identification of compound **37-1** (TRKA kinase IC_{50} = 0.011 μ M, cell IC_{50} = 0.003 μ M). Figure 24B illustrates the binding mode of **37** with TRKA.¹⁷³ It is clear from this study that the compound bound to =TRKA in a DFG-out conformation, which is a typical feature for amide- and urea-linked Type II kinase inhibitors. However, **37** is structurally unlike any known Type II TRK inhibitor because of its low molecular weight and simple architecture.¹⁷³ At the ATP-binding site, the thiazole heterocycle forms a very weak hydrogen bond (3.45 Å) with the amide backbone of Met592. The benzylic ring is involved in hydrophobic interactions with the gatekeeper residue, Phe589. The para-trifluoromethoxyphenyl group occupies the hydrophobic pocket normally occupied by Phe669 in the DFG-in conformation. The amide carbonyl forms a hydrogen bond with Asp668 as is typical with most Type II kinase inhibitors.¹³⁷ A highly unique attribute to **37** is the cyclopropyl group, which occupies a hydrophobic cleft and is tucked

against Val524. This is an uncommon trait, as most kinase inhibitors are unsubstituted at this position and hydrogen bond to a glutamic acid on the α -C-helix.¹⁷³ One interpretation of the cyclopropyl SAR is that a critical hydrophobic mass is required to fill a small pocket near Val524 and Phe589. The placement of a hydrophobic group at this region is hypothesized to displace water, which would otherwise occupy the area.¹⁷³ These interactions suggest the compound exhibits binding properties more typical of a Type III inhibitor.

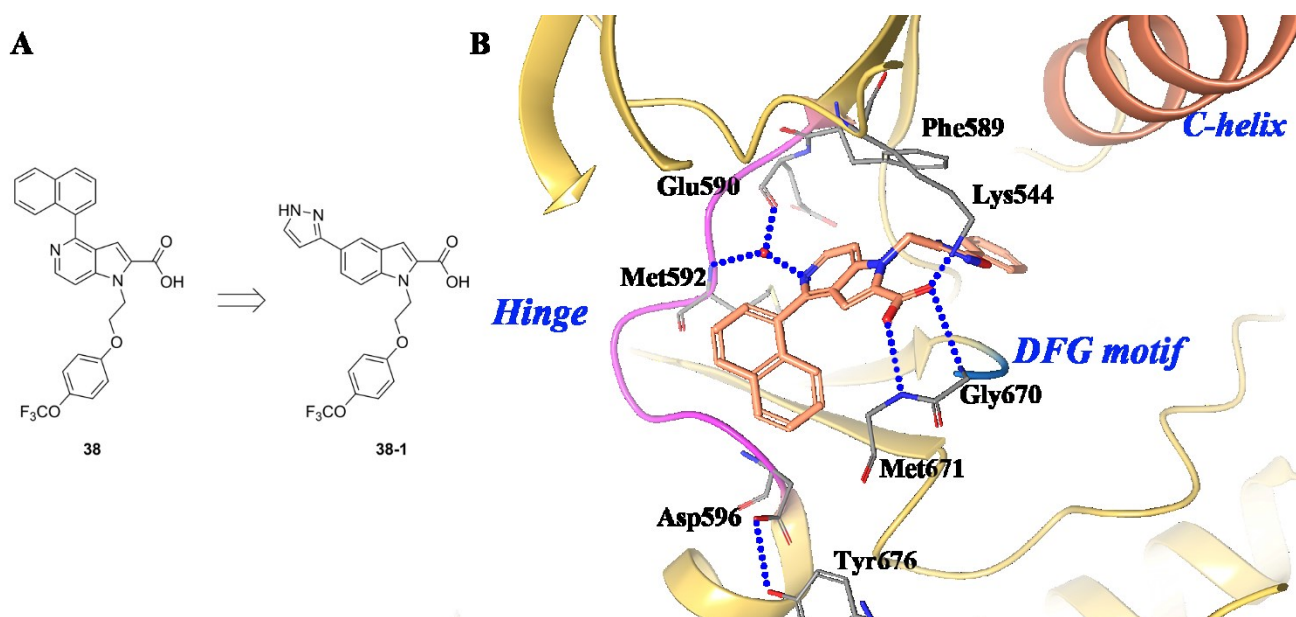


Figure 25. (A) Identification of compound **38-1**; (B) Co-crystal structure of compound **38** and its binding mode in TRKA (PDB ID: 4PMS, 2.8 Å). The kinase is depicted in yellow ribbons and the hydrogen bonds are illustrated in blue dashed lines.

In the same manuscript by Stachel *et al.*, the author discussed the development of compound **38** (TRKA kinase IC_{50} = 17.13 μ M, cell IC_{50} = 1.162 μ M) to compound **38-1** (TRKA kinase IC_{50} = 0.051 μ M, cell IC_{50} = 0.029 μ M) (Figure 25A).¹⁷³ Compound **38** was shown to bind to the DFG-out conformation of TRKA (Figure 25B).¹⁷³ The co-crystal structure revealed several unusual binding features. First, no direct interaction between the hinge backbone and the inhibitor was identified. Instead, the N5 nitrogen from the azaindole was shown to participate in a water-mediated hydrogen bond to the hinge region.¹⁷³ The naphthalene moiety was buried in the hydrophobic cleft at the front of the hinge

flanked by the activation loop residue Met671. One of the more unusual binding features is that the indole carboxylic acid interacts with two backbone amides in the activation loop. The unique interactions at the hinge and the activation loop regions anchor **38** to the ATP binding site. A third interaction was also evident between the carboxylic acid and Lys544 on the roof of the ATP binding pocket.¹⁷³ Compound **38** exhibited phosphorylation-dependent binding, which was due to the unusual conformation between the indole carboxylic acid and the activation loop. In the co-crystal structure, Tyr676 was involved in a hydrogen-bond interaction with Asp596. Since Tyr676 is a known phosphorylation site on TRKA, phospho-Tyr676 would disrupt this interaction with Asp596, forcing the activation loop away from the active site and stabilizing the active conformation. As such, the phosphorylated form of the enzyme is not able to bind compound **38**.¹⁷³ Because of the highly unique binding of **38** to TRKA, the compound exhibits a profile more typical of Type III.

Type III-JM TRK Inhibitors

TRKA activation triggers intracellular signaling cascades that increase the sensitivity of nociceptors, thus leading to chronic sensitization and pain.²⁰⁰ However, TRKA/B/C share significant sequence homology at the kinase domain, which will make it extremely difficult to develop inhibitors selective for a single isoform. A method to circumvent selectivity issues is to develop allosteric inhibitors that do not bind to the highly conserved ATP active site. In an effort to identify TRKA specific inhibitors, Su *et al.* discovered compounds with novel scaffolds that bound to the juxtamembrane (JM) domain of TRKA.¹³⁸ The JM domain is located between the kinase domain and the transmembrane domain, and there is only 36% identity between TRKA and TRKB and 40% identity between TRKA and TRKC.¹³⁸ These findings provide the research community with a novel, exploitable region to generate TRK selective small molecule inhibitors.

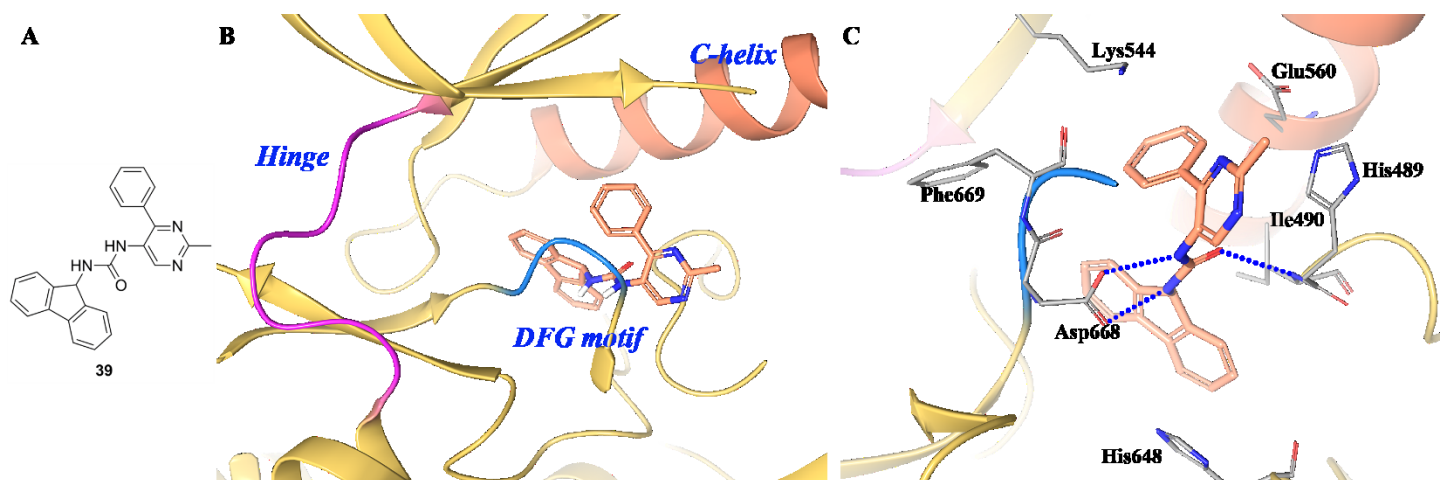


Figure 26. (A) Chemical structure of compound **39**; (B) Co-crystal structure of compound **39** in the allosteric pocket of TRKA (PDB ID: 5KMI, 1.87 Å); (C) Interactions of compound **39** with surrounding residues. The kinase is depicted in yellow ribbons and the hydrogen bonds are illustrated in blue dashed lines.

Compound **39** is a selective TRKA inhibitor (IC_{50} s for TRKA/B/C were 0.099 μ M, > 81 μ M and 25 μ M, respectively) (Figure 26A).¹³⁸ In the co-crystal structure of **39** and TRKA (Figure 26B and Figure 26C), compound **39** bound behind the DFG motif opposite of the kinase active site.¹³⁸ The DFG motif was found in a DFG-out, inactive conformation, with Phe669 pointed toward the active site. Asp668, which coordinates to the phosphate groups on ATP, is away from the active site in the structure. The central urea of compound **39** makes two hydrogen bonds with Asp668. Asp668 is part of the DFG motif, and binding to compound **39** requires the DFG motif to be in the ‘out’ conformation.¹³⁸ The fluorine moiety of compound **39** occupies a relatively hydrophobic pocket formed primarily by aliphatic amino acids. The structure clearly reveals interactions at the JM region. Ile490, within the JM, sits on top of the fluorine moiety, aiding to the formation of the hydrophobic pocket.¹³⁸ Similar to other TRKA co-crystal kinase structures, there is a shift in Phe646, which creates a pocket to accommodate the fluorine. The oxygen of the central urea in compound **39** forms a hydrogen bond with the amide nitrogen of Ile490. The phenyl moiety occupies a position between Lys544 of the β 3 strand and Glu560 of the α -C-Helix.¹³⁸

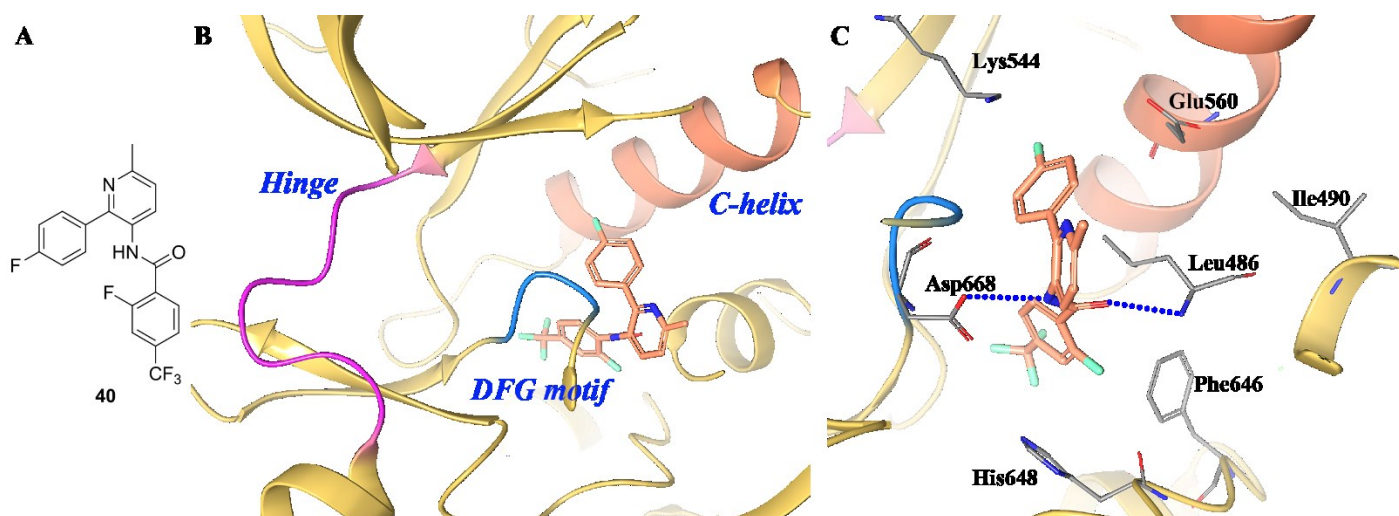


Figure 27. (A) Chemical structure of compound **40**; Co-crystal structure of compound **40** in the allosteric pocket of TRKA (PDB ID: 5KMK, 1.65 Å). (C) Interactions of compound **40** with surrounding residues. The kinase is depicted in yellow ribbons and the hydrogen bonds are illustrated in blue dashed lines.

Compound **40** is another selective TRKA inhibitor with interesting binding features (IC_{50} s for TRKA/B/C were 3.3 μ M, >81.0 μ M, and 27 μ M, respectively) (Figure 27A).¹³⁸ The co-crystal structure of compound **40** revealed the compound bound to the same pocket as **39**, behind the DFG motif (Figure 27B and Figure 27C). The trifluorophenyl moiety of **40** sits in the pocket occupied by the fluorine of compound **39**. The central amide nitrogen is positioned close to the carboxylic acid of Asp668. The binding site is quite similar between the two structures except for the following differences: (1) for compound **39**, Ile490 packs above the phenyl ring, but Leu486 packs above the phenyl ring for **40**; (2) for **39**, Phe646 was displaced by the bulky moiety in the hydrophobic pocket, but for **40**, the smaller moiety accommodates Phe646 in a position closer to the active conformation.¹³⁸

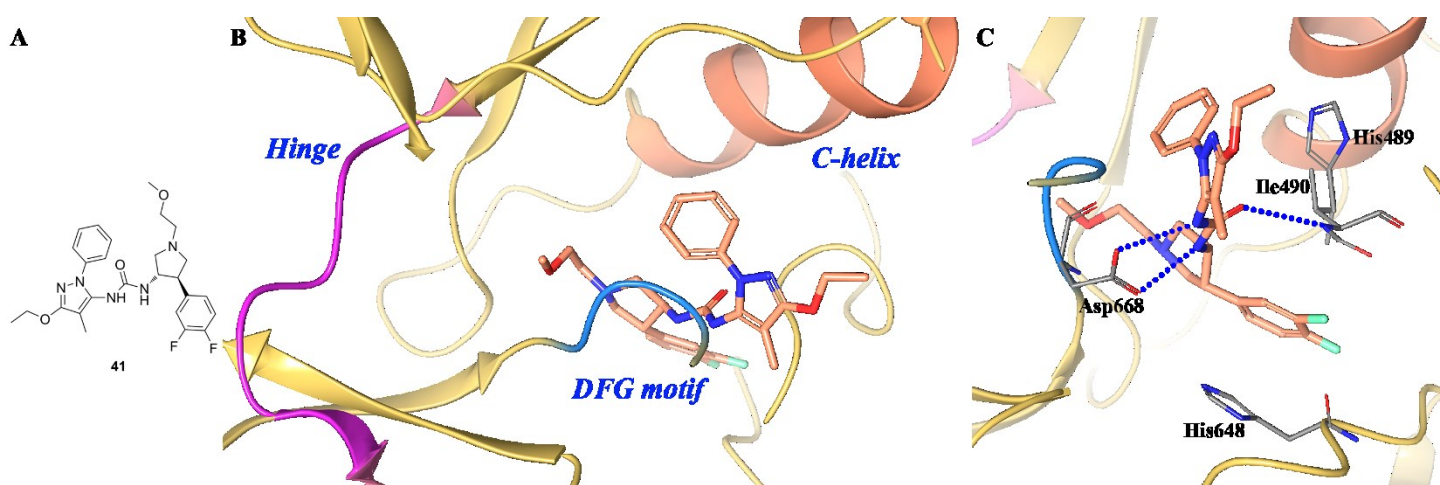


Figure 28. (A) Chemical structure of compound **41**; (B) Co-crystal structure of **41** bound in the allosteric pocket of TRKA (PDB ID: 5H3Q, 2.1 Å); (C) Interactions of compound **41** with surrounding residues. The kinase is depicted in yellow ribbons and the hydrogen bonds are illustrated in blue dashed lines.

A similar finding was also disclosed by Furuya *et al.*²⁰⁰ Compound **41** (Figure 28A) showed potent inhibitory activity against TRKA (IC_{50} = 0.0027 μ M) but was selective against TRKB and TRKC (IC_{50} s were 1.3 μ M and 2.5 μ M, respectively). Figure 28B and Figure 28C illustrate that compound **41** bound to the JM region of TRKA. The

configuration of the kinase domain and A loop is very similar to that observed for Apo TRKA.²⁰⁰ **41** binds to the deep pocket formed by the DFG region of the A loop, glycine-rich loop (G loop), C-helix, and JM region. This pocket is completely separate from the ATP site. There are four key interactions that **41** creates at the binding region: (1) Asp668 of the DFG motif forms two hydrogen bonds with the urea moiety; (2) His489 interacts with the pyrazole ring via π - π interactions and with the ethoxy group via CH- π interactions; (3) Ile490 forms a hydrogen bond with the urea moiety and interacts with the difluorobenzene group of **41** via CH- π interactions; (4) His648 interacts with the difluorobenzene moiety through a π - π stacking interaction.²⁰⁰ In addition to these, Leu486 is also involved in weak Van der Waals interactions with the methyl and ethoxyl groups of **41**. Interestingly, these amino acid residues are not conserved in TRKB nor TRKC but are integral for high binding affinity in TRKA.²⁰⁰ Further exploitation of these TRKA specific amino acids could furnish numerous allosteric scaffolds with high TRKA selectivity.

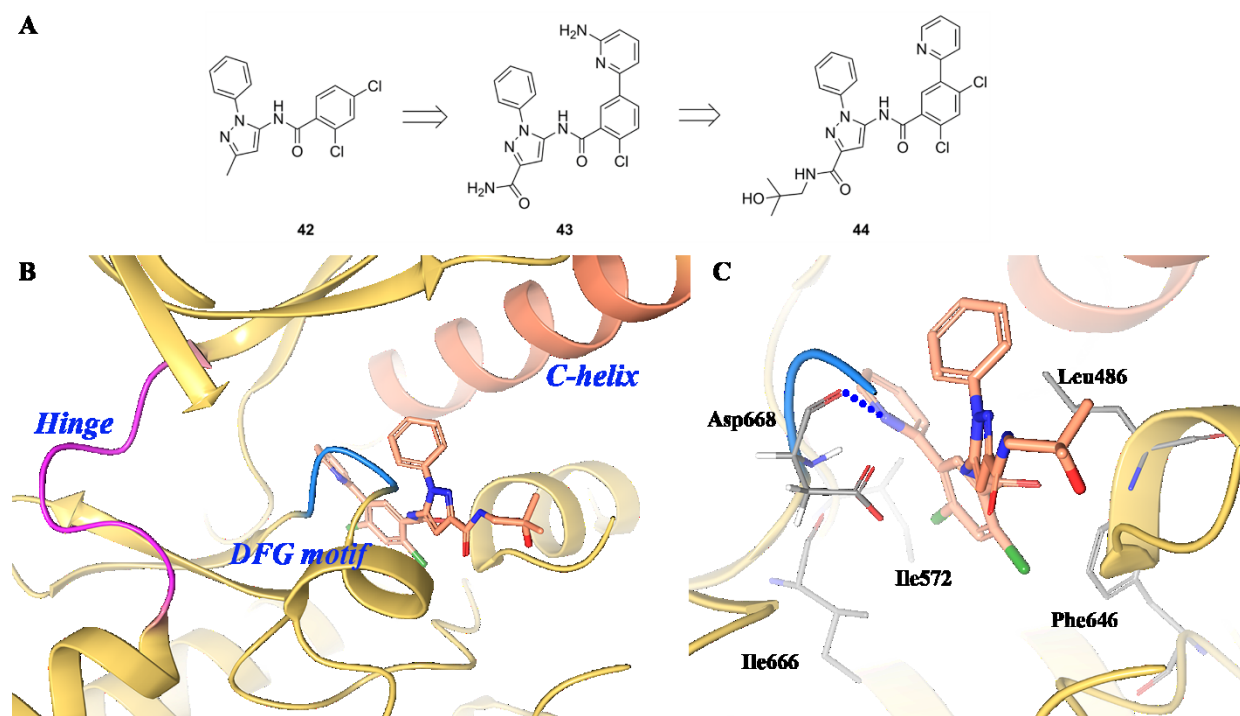


Figure 29. (A) Chemical structures of compounds **42**, **43**, and **44**; (B) Co-crystal structure of compound **44** bound to the allosteric pocket of TRKA (PDB ID: 6D20, 1.94 Å); (C) Interactions of compound **44** with surrounding residues. The kinase is depicted in yellow ribbons and the hydrogen bonds are illustrated in blue dashed lines.

Recently, Bagal *et al.* reported the discovery of a series of N-phenyl-pyrazole based compounds as selective TRKA inhibitors (Figure 29A).²⁰¹ The original hit **42** showed moderate TRKA inhibitory activity (TRKA cell IC₅₀ = 3.3 μM) and >10-fold selective over TRKB/C (TRKB/C cell IC₅₀s > 50 μM). By introducing an amino-pyridine ring to the dichloro-phenyl ring and switching the methyl to an amide group, the resultant compound **43** demonstrated 66-fold improvement in TRKA potency (cell IC₅₀ = 0.05 μM) and was >80-fold selective over TRKB/C (Cell IC₅₀s were 14 μM and 4.1 μM, respectively) with improved drug-like properties.¹⁸⁶ A variety of functional groups were evaluated on the pyridine and central phenyl ring, which led to the identification of **44** (TRKA/B/C IC₅₀s = 0.01 μM, 1.8 μM, and 0.7 μM, respectively) (Figure 29A). Compound **44** showed <15% inhibition against a panel of over 390 kinases at a concentration of 10 μM and was 72% orally bioavailable.²⁰¹ Figure 29B and Figure 29C illustrate the binding mode of **44** in the allosteric pocket of TRKA. The pyridyl nitrogen forms a hydrogen bond with the backbone of Asp668. The di-chloro central phenyl ring occupies the lipophilic pocket surrounded by Leu486, Ile572, Phe646 and Ile666. The terminal carbonyl group interacts with the side chain of Arg673 and the tertiary alcohol is exposed to the solvent front.²⁰¹

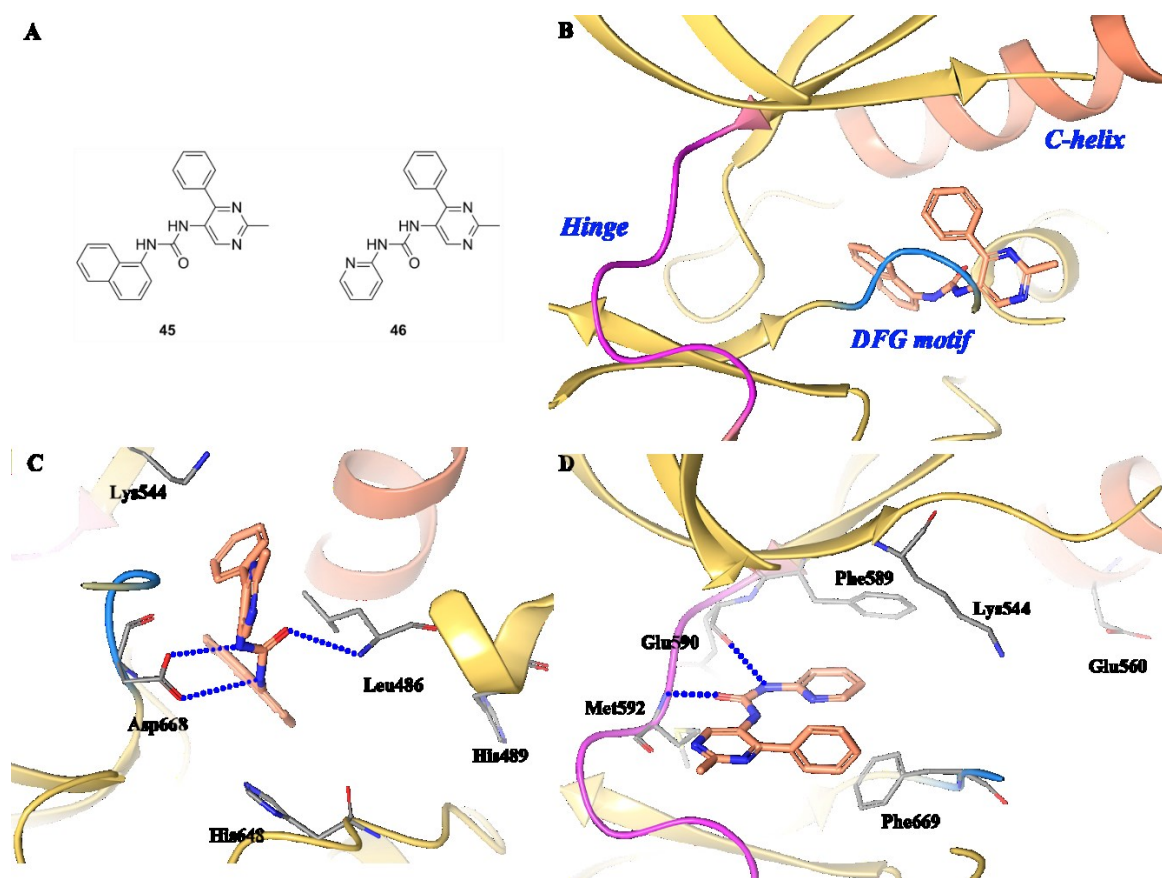


Figure 30. (A) Chemical structures of compounds **45** and **46**; (B) Co-crystal structure of compound **45** binding in the allosteric pocket of TRKA (PDB ID: 5KMM, 2.1 Å); (C) Interactions of compound **45** with surrounding residues; (D) Co-crystal structure of compound **46** in the active site of TRKA (PDB ID: 5KMO, 2.7 Å). The kinase is depicted in yellow ribbons and the hydrogen bonds are illustrated in blue dashed lines.

However, it is worth noting that two analogues of **39**, compounds **45** and **46** (by switching the fluorine moiety to naphthalene or pyridine), were also reported by Su *et al.* (Figure 30A).¹³⁸ These two compounds were active against TRKA and TRKC (**45**, TRKA/C IC₅₀s = 4.1 μM and 7.1 μM, respectively; **46**, TRKA/C IC₅₀s = 4.0 μM and 2.3 μM, respectively). Interactions of compound **45** with the kinase domain are similar to **39** but the JM interactions are altered as His489 is shifted away from the compound (Figure 30B and Figure 30C). Instead of binding to the allosteric pocket, **46** binds to the active site in an atypical Type I conformation (Figure 30D). The urea carbonyl group forms a hydrogen bond with the hinge residue Met592, and the pyridine fragment has a weak π - π interaction with the DFG motif residue Phe669.¹³⁸ In this case, it is still uncertain whether compounds with such scaffolds will exhibit TRKA selectivity. It could be expected that only a subset of Type III inhibitors could be TRKA-selective because specific JM domain interactions are required for inhibition.¹³³

Beyond compounds described above, there are three additional TRK inhibitors under clinical development with structures that have not been disclosed. These compounds include **PLX7486** (NCT01804530), **DS-6051B** (NCT02279433), and **F17752** (2013–003009–24).

Clinical Evaluation of TRK Inhibitors

Table 2. Reported drugs under clinical trials with known inhibitory activity of TRK kinases

NCT Identifier	Phase	Therapeutic Agent	Indication	Status	Patient Selection	Estimated Completion
NCT03213704	Phase II	Larotrectinib (8)	Pediatric Cancers	Recruiting	NTRK gene fusions	09/2024
NCT02637687	Phase II	Larotrectinib (8)	CNS Cancers	Recruiting	/	06/2019
NCT02576431	Phase II	Larotrectinib (8)	NTRK+ Solid Tumors	Recruiting	NTRK gene fusions	04/2018
NCT02122913	Phase I	Larotrectinib (8)	Solid Tumors	Recruiting	NTRK gene fusions	02/2017
NCT03215511	Phase I/II	LOXO-195 (9)	TRK Resistant Tumors	Recruiting	TRK-resistant lesions	08/2019
NCT02568267	Phase II	Entrectinib (4-3)	Solid Tumors	Recruiting	NTRK, ROS1, or ALK	10/2019

					gene rearrangements	
NCT02097810	Phase I	Entrectinib (4-3)	Advanced/Metastatic Cancer	Active	NTRK, ROS1, or ALK molecular alterations	06/2019
NCT02650401	Phase I	Entrectinib (4-3)	Pediatric and CNS Cancers	Recruiting	With or without NTRK, ROS1, or ALK gene fusions	08/2018
NCT01639508	Phase II	Cabozantinib (23)	Advanced NSCLC	Recruiting	RET, ROS1, or NTRK fusions or increased MET or AXL activity	07/2019
NCT02048488	Phase I/IIa	Belizatinib (5-3)	Solid Tumors and Lymphomas	Unknown	/	09/2016 ⁺
NCT02279433	Phase I	DS-6051b	Advanced Solid Tumors	Active	NTRK or ROS1 gene rearrangements	11/2019
NCT02675491	Phase I	DS-6051b	Advanced Solid Tumors	Active	NTRK or ROS1 gene rearrangements	09/2018
					MET, NTRK, or DDR2 mutations, MET or KIT/PDGFR/VEGFR2 gene amplification,	
NCT02219711	Phase I	Sitavatinib (24)	Advanced Cancers	Recruiting	MET, RET, AXL, NTRK1, or NTRK3 gene rearrangements, or CBL gene function mutations loss	12/2018
NCT01804530	Phase I	PLX7486	Advanced Solid Tumors	Terminated	NTRK point or fusion mutations	01/2018*
NCT02228811	Phase I	Altiratinib (25)	Advanced Solid Tumors	Terminated	NTRK or MET gene alterations	11/2017*

+ Study has passed its completion date and status has not been verified in more than two years

*Actual Primary Completion Date

All TRK-directed compounds under clinical investigation are pan-TRK inhibitors. This is likely due to the conservation of amino acids at the ATP binding domain of TRK isoforms. Pivotal TRK structural analysis completed by Bertrand, *et al.* only identified a two amino acid difference between the ATP binding site of TRKA and TRKB.⁷³ When analyzing TRKB and TRKC, all ATP binding site residues were identical.⁷³ Because all TRK inhibitors in clinical trials elicit activity by binding at the ATP binding site, they all possess pan-TRK activity. This activity profile is possibly beneficial because the inhibitors, in theory, can be utilized against a broad spectrum of tumors. However, this must be vetted cautiously, as dose-limiting toxicity can also increase based on inhibition profiles. An extensive, clinical overview for the development of TRK inhibitors has been reviewed by Lange, et al.²⁰²

Larotrectinib (**8**, LOXO-101) is under clinical investigation to treat melanoma, glioblastoma, NSCLC, pancreatic and ovarian cancers, and pediatric cancers. Following a single, oral dose, the unbound plasma concentration of

larotrectinib is sufficient to inhibit TRKA/B/C signaling without substantial inhibition of other kinases.²⁰³ In a phase I study with larotrectinib, six patients with *NTRK* fusions with heavily pretreated advanced disease were enrolled (NCT02122913).²⁰⁴ Of the six patients, three had partial responses within 3-4 months and one patient had a near-complete response after 8 months.¹⁵⁷ The drug was well tolerated, and the main side effects were fatigue, dizziness, and anemia. Larotrectinib was even well tolerated and efficacious in pediatric carcinomas harboring a TRK oncogene.²⁰⁵⁻²⁰⁶ Due to the overall positive results of the phase I study, Bayer and Loxo Oncology initiated a multicenter phase II basket trial to evaluate larotrectinib in patients with an *NTRK* fusion oncogene (NCT02637687 and NCT02576431). The overall response rate to treatment was 75%, with 13% exhibiting a complete response.⁹⁹ At 1 year, 55% of the treated patients remained progression free. Based on the phase II results, larotrectinib has marked and durable antitumor efficacy in patients with *NTRK* fusions, regardless of age or tumor origin.^{99, 207} Meeting future endpoints of clinical trials, such as median duration of response, progression-free survival, and overall survival, will further confirm the clinical utility of larotrectinib.

Entrectinib (**4-3**, RXDX-101) is a pan-kinase inhibitor under clinical development by Ignyta with activity against TRKA/B/C, ROS1, and ALK fusion oncogenes.¹⁴⁹ In a phase 1 clinical trial, 119 patients were treated with entrectinib split between two subgroups: ALKA-372-001, 54 patients, and STARTRK-1, 65 patients (NCT02097810).²⁰⁸ Entrectinib was shown to be well tolerated and efficacious against *NTRK1/2/3* and *ALK* gene fusions, including patients with primary or secondary CNS disease.²⁰⁸ The majority of treatment related toxicities were Grades 1-2 and reversible with cessation or modification of treatment.²⁰⁸ In particular, responses were achieved regardless of histology, with responses observed in NSCLC, MASC, melanoma, glioneuronal tumor, colorectal cancer, and RCC.²⁰⁸ Response rates were highest in *NTRK*-rearranged tumors, which provided first-time, clinical ‘proof-of-concept’ that *NTRK*-rearrangements are actionable drivers of tumor growth.²⁰⁸ Because of the success of phase 1 studies, a global, multicenter phase II basket study (STARTRK-2) is currently recruiting patients with *NTRK*-, *ROS1*-, and *ALK*-rearranged tumors (NCT02568267).²⁰⁹ These studies are being performed to confirm the results of the phase 1 study and to further establish the safety profile of entrectinib in a larger patient population. The clinical success of the phase 2 studies relies on the successful enrichment of patients with targetable gene fusions. Because of the rarity of *NTRK*-rearranged tumors and the success of the phase 1 trial, patients are being enrolled based on molecular, rather than histological, criteria.

Sitravatinib (**24**, MGCD516) is a multi-kinase inhibitor under clinical development by Mirati Therapeutics Inc. with activity against RTKs including MET, AXL, MER, and members of the VEGFR, PDGFR, DDR2, TRK and Eph families.¹⁹⁰ A phase 1/1b study is currently recruiting to evaluate dose and preliminary efficacy in patients harboring gene rearrangements involving *MET*, *RET*, *AXL*, or *NTRK1/2/3* (NCT02219711).²¹⁰ Based on pre-clinical data, sitravatinib is likely to be effective for metastatic, soft-tissue sarcomas. Similar to entrectinib, the clinical success of sitravatinib will rest on the ability to appropriately enrich patients for targetable, molecular lesions. Although blockade of multiple driver signaling pathways can be achieved with sitravatinib,¹⁹⁰ clinical investigation must identify a therapeutic window to safely target *NTRK* rearrangements without breaching dose-limiting toxicity on other kinase pathways.

DS-6051b is under clinical development by Daiichi Sankyo, Inc. for advanced solid tumors harboring *ROS1* or *NTRK1/2/3* rearrangements. A phase 1, two-part clinical trial is underway to determine dose-limiting toxicities and tumor response for up to two years (NCT02279433). Results from a phase 1 trial in Japanese subjects have already been published with dose-limiting toxicities experienced at the highest dose of 800 mg QD (NCT02675491).²¹¹ Tolerability in American subjects was similar, with dose-limiting toxicities experienced at 800 and 1,200 mg QD.²¹² Partial responses, based on tumor regression, were observed at or above the maximum tolerated dose warranting additional safety studies and better patient enrichment for a more durable, clinical response.

Cabozantinib (**23**, COMETRIQ®) is a pan-kinase inhibitor developed by Exelixis with FDA approval to treat metastatic medullary thyroid cancer (mMTC) and renal cell carcinoma (RCC). Cabozantinib was first approved to treat mMTC in 2012 and later, in 2016, it was approved for RCC. Because of its pan-kinase profile demonstrating activity against c-Met, RET, ROS1, ALK, VEGFR2, and TRK receptors, cabozantinib is under phase II clinical investigation for patients harboring *NTRK1* gene fusions in NSCLC (NCT01639508). In the same trial, the drug is being evaluated against patients with RET, ROS1, MET, and AXL oncogenes. Cabozantinib has been found to increase the risk of gastrointestinal perforations, fistulas, and hemorrhage and carries a black box warning for these side effects. In head-to-head studies, entrectinib exhibits stronger inhibition of *NTRK* fusion genes compared to cabozantinib, which suggests the clinical utility of entrectinib might be greater.¹⁶¹ Further, cabozantinib inhibits VEGFR2 at an IC_{50} of $0.000035 \mu M$ ²¹³ and other tyrosine kinases $>0.001 \mu M$, which positions cabozantinib as a highly potent, selective, and unique VEGFR2 inhibitor. The clinical utility of an inhibitor with strong VEGFR2 selectivity must be further evaluated for usefulness against TRK-

driven disease. Because of the pan-kinase profile of cabozantinib, clinical response against TRK cancers can be robust, but this also must be weighed against the high propensity for DLTs. Phase II clinical investigation will further evaluate the usefulness of cabozantinib in safely treating TRK-driven cancers.

A major clinical consideration for TRK inhibitors is the propensity to select for drug resistant TRK mutations. For example, a metastatic colorectal cancer patient harboring a *NTRK1* gene fusion displayed a marked response to entrectinib.¹⁶⁰ However, after 4 months of treatment, entrectinib lost effectiveness in controlling tumor growth. By monitoring circulating tumor DNA (ctDNA), it was identified that the TRKA kinase domain underwent two different point mutations at G595R and G667C. These point mutations were also shown to limit the TRKA inhibitory activity of larotrectinib and belizatinib.¹⁶⁰ To overcome TRK resistant mutations, LOXO-195 (**9**) was developed, which is a constrained analogue of larotrectinib. Due to conformational limitations, steric interactions with TRKA G667C and TRKC G623R (homologous to TRKA G595R) are limited and kinase inhibitory activity is maintained. These results have been translated into clinical trials where patients have responded to LOXO-195 after failing treatment with larotrectinib.¹⁵⁹ Clinical trials for LOXO-195 are ongoing and are displaying the potential to extend durable remissions in patients with TRK-resistant lesions (NCT03215511).

Conclusion and Future Perspective for TRK Inhibitors

The use of kinase-directed precision medicine has been heavily pursued since the discovery and development of imatinib.⁴² Kinases have since emerged as one of the most intensely pursued drug targets in oncology research due to highly druggable active sites and their critical roles in cellular signaling. However, there has yet to be a clinically approved inhibitor for the TRK-receptor tyrosine kinase despite its intimate involvement in tumor pathology and disease. The vast majority of kinase inhibitors developed for TRK exhibit limited selectivity against any of the three isoforms (TRKA/B/C) and are active in the greater kinome. These types of inhibitors will have limited utility as tools to further study TRK biology but have exhibited excellent therapeutic potential in clinical trials, especially when patients treated with TRK inhibitors are selected based on their molecular pathology. To further study TRK biology, it will be beneficial to utilize highly selective inhibitors with activity specific for a single, TRK isoform, such as **41** for TRKA. This will permit the inhibition of a single enzyme in the TRK family, which can help identify isoform importance and interplay in a variety of preclinical TRK-models. It is important to note that TRK signaling, specifically via their corresponding growth

factors,²¹⁴ has been implicated in mediating and modulating the pain response. As such beyond cancer, TRK inhibitors are being evaluated in clinical trials as agents to reduce neuropathic pain (NCT03346330).

The most clinically advanced TRK inhibitors include entrectinib, a pan-TRK, ALK and ROS inhibitor, and larotrectinib, a specific, pan-TRK inhibitor. Both larotrectinib and entrectinib have achieved orphan designation from regulatory authorities.⁴⁸ A recent report of the clinical activity of entrectinib in 55 TRK mutant patients displayed an 80% overall response rate with long-lasting responses in 71% of patients (> 12-months).¹⁰⁰ An aspect that needs to be considered in the development of TRK inhibitors is, given their role in the nervous system, the possibility of adverse neuropsychiatric effects. One parameter that may influence this property is activity in the greater kinome and, another, the ability to cross the blood-brain barrier. Noteworthy, the most advanced TRK inhibitors under clinical development, such as larotrectinib and entrectinib, exhibited neurotoxicity. This is likely due to target specificity, although they are able to penetrate the blood-brain barrier and exert therapeutic effects against brain metastases.⁴⁸ The identification of the clinical candidate PF-06273340 (**22-3**) provides a strategy to deliver peripherally restricted and orally bioavailable compounds, which was to design compounds in physicochemical space appropriate for absorption across the gastrointestinal epithelium while, simultaneously, engineering the compounds as substrates for blood–brain barrier efflux transporters.^{186,}

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As observed with all kinase inhibitors, TRK resistance to precision medicine is a major therapeutic limitation for durable efficacy. To overcome resistance, LOXO-195 was developed and is exhibiting effectiveness to induce remissions in patients that have failed larotrectinib treatment. The exact duration of remission is being investigated in clinical trials, and the development of LOXO-195 is a hopeful addition for treating TRK-driven disease. Clinical studies have confirmed the importance of selecting patients based on molecular criteria, and this enrichment will become even more important when transitioning from 1st to 2nd generation TRK inhibitors. Although all evaluation of TRK precision medicine is in the early stages of clinical development, significant breakthroughs have been uncovered for the treatment and management of TRK-driven tumors. With the completion of clinical studies incorporating larger patient populations it is expected that TRK precision medicine will continue to exhibit efficacy. Larger clinical studies will also illuminate if selective (larotrectinib) or pan-kinase inhibitors (entrectinib) are more appropriate for treating TRK malignancies. With the advent of routine molecular profiling of tumors, patients will be treated with TRK precision medicine to induce a

tailored response. This will translate to customized treatment profiles that will better target the unique pathology of a patient's tumor.

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Notes

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Abbreviations used

AKT, v-akt murine thymoma viral oncogene homologue; ALIS, automated ligand identification system; ALK, anaplastic lymphoma kinase; AML, acute myeloid leukemia; ATP, adenosine triphosphate; BDNF, brain-derived neurotrophic factor; CDK, cyclin-dependent kinase; CML, chronic myelogenous leukemia; DAG, diacyl-glycerol; DDR2, Discoidin domain-containing receptor 2; ERK, extracellular signal-regulated kinase; FDA, food and drug administration; FLT3, fms-like tyrosine kinase 3; Glio, glioblastoma; GRB2, growth factor receptor-bound protein 2; hERG, human ether-a-go-go-related gene; IC, intrahepatic cholangiocarcinoma; IGF1R, insulin-like growth factor 1; IP3, inositol trisphosphate; MASC, mammary analogue secretory carcinomas; MEK, mitogen-activated protein kinase; NGF, nerve growth factor; NT3, neurotrophin-3; PH, pleckstrin homology; PI3K, phosphatidylinositol-4,5-bisphosphate 3-kinase; PLC γ , phospholipase C- γ ; PKC, protein kinase C; PTC, papillary thyroid cancer; PDGFR, Platelet-derived growth factor receptor; P-gp, P-glycoprotein; QSAR, quantitative structure–activity relationship; RAF, rapidly accelerated fibrosarcoma oncogene; RAS, rat sarcoma oncogene; RET rearranged during transfection; Ron, recepteur d'origine nantais;; RTK, receptor tyrosine kinases; SHC, Src homology 2 domain containing; TIE-2, tunica interna endothelial-2; TRK, tropomyosin receptor kinase; VEGFR2, vascular endothelial growth factor receptor 2;

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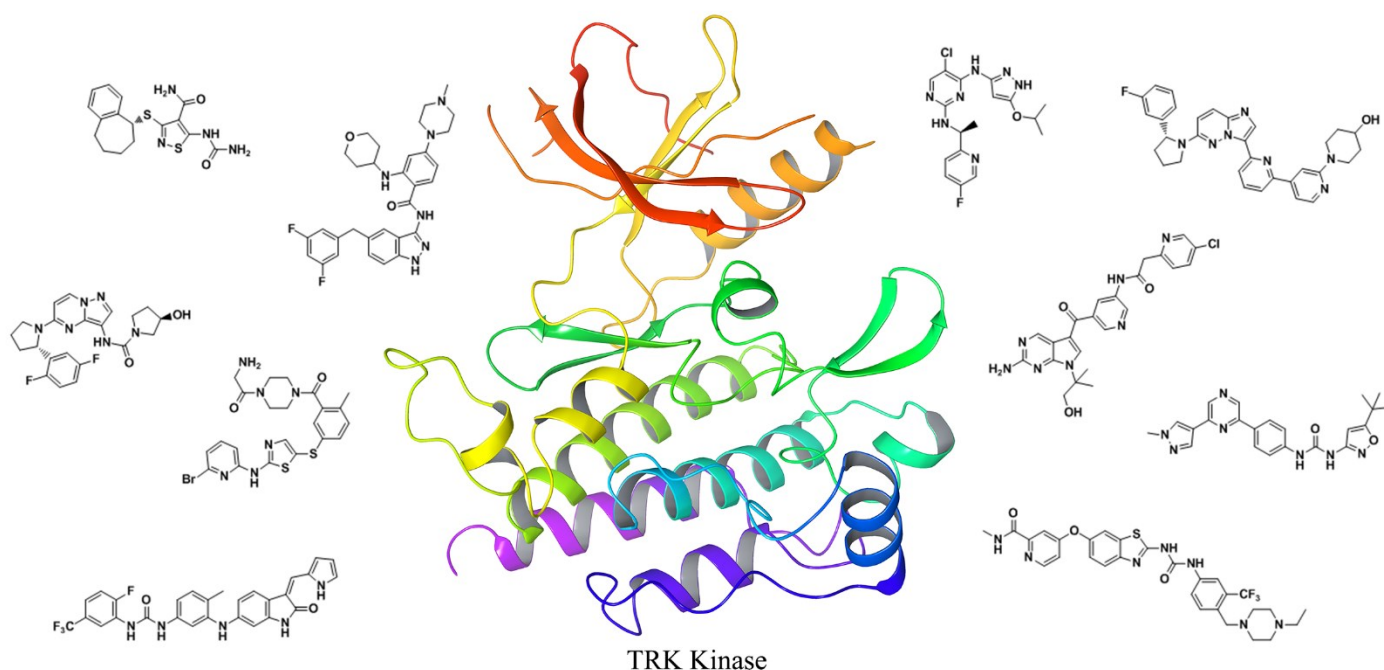


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